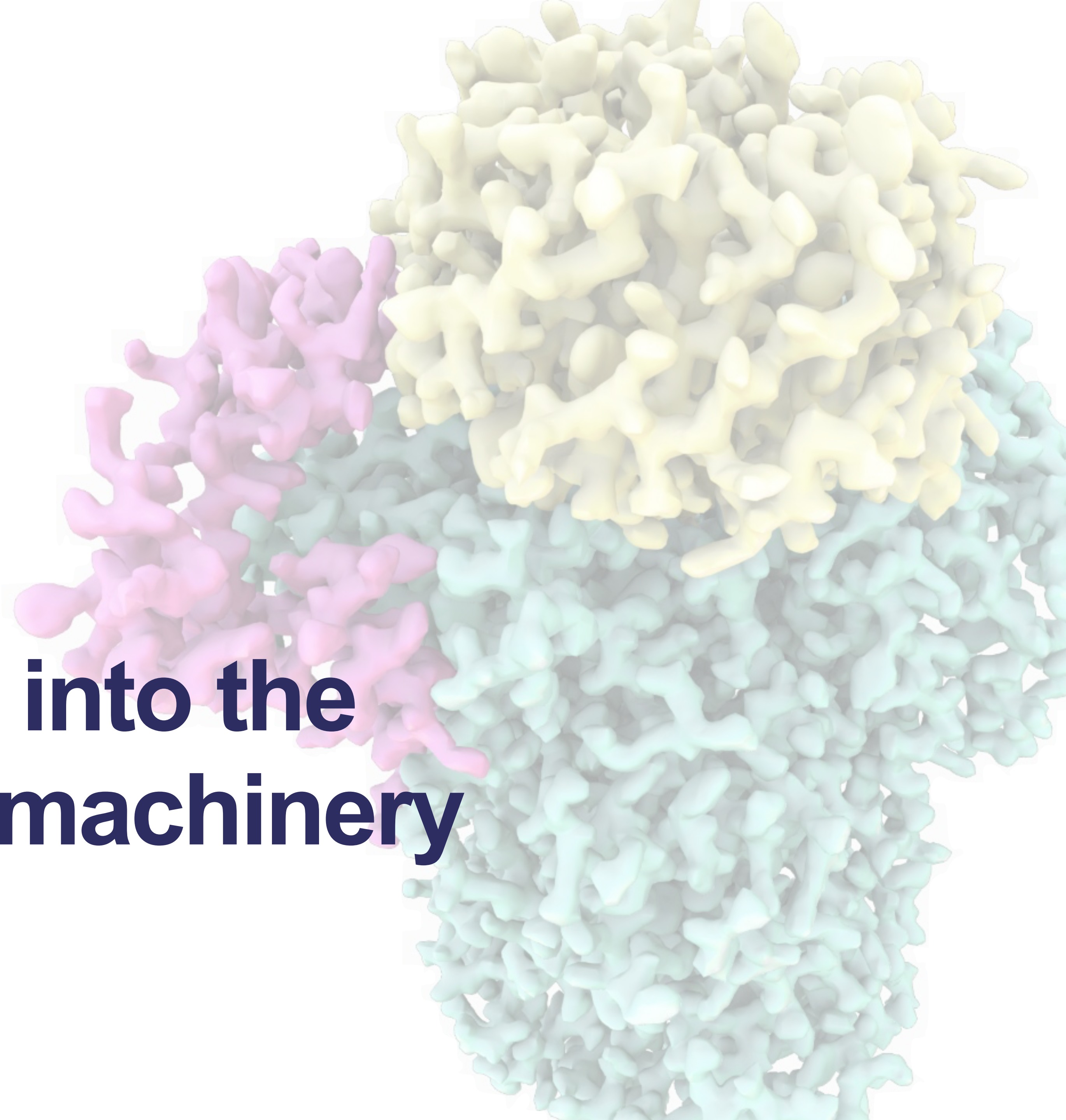




MRC Laboratory
of Molecular
Biology

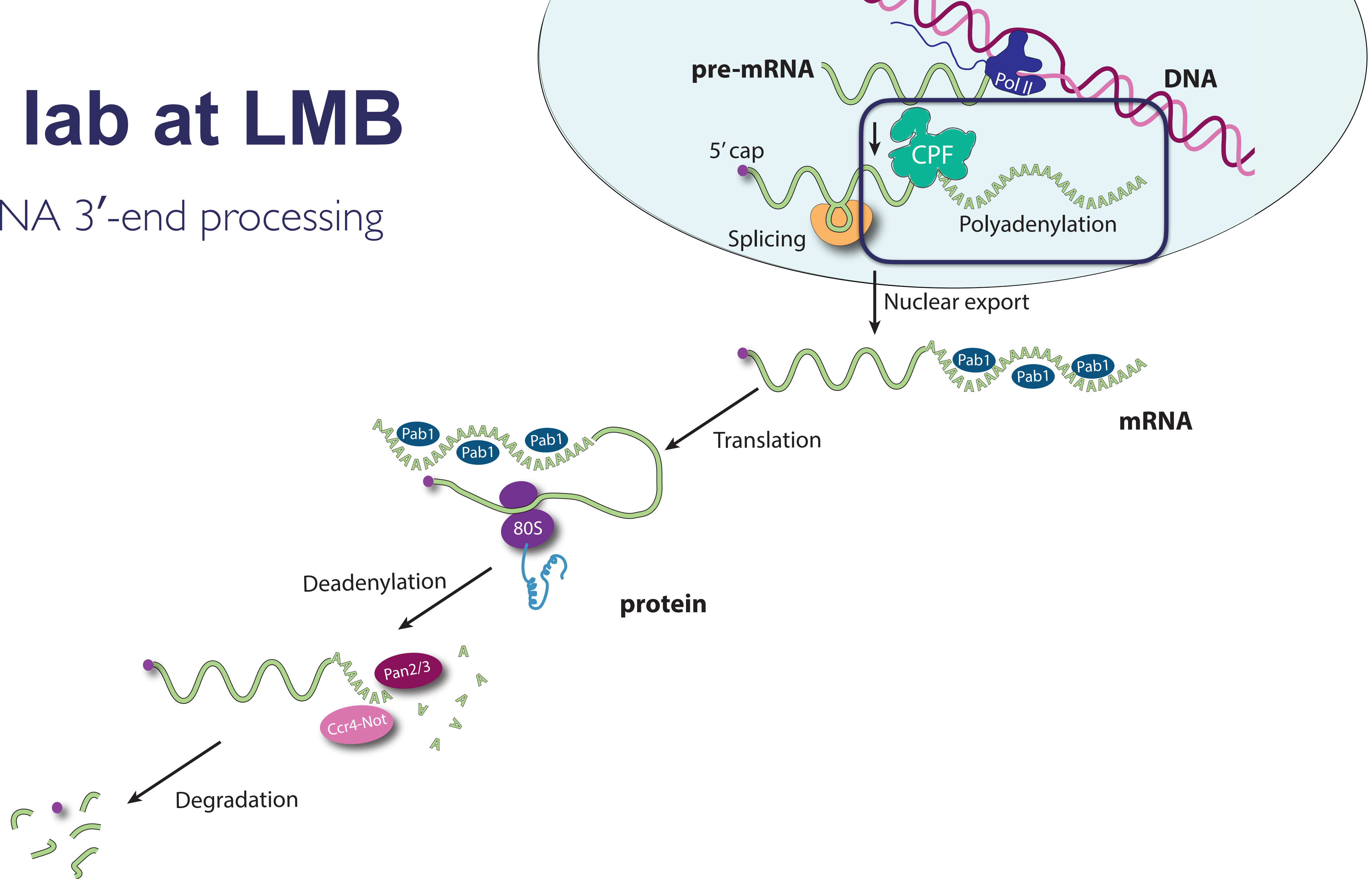
Molecular insights into the mRNA poly(A) tail machinery

Lori Passmore



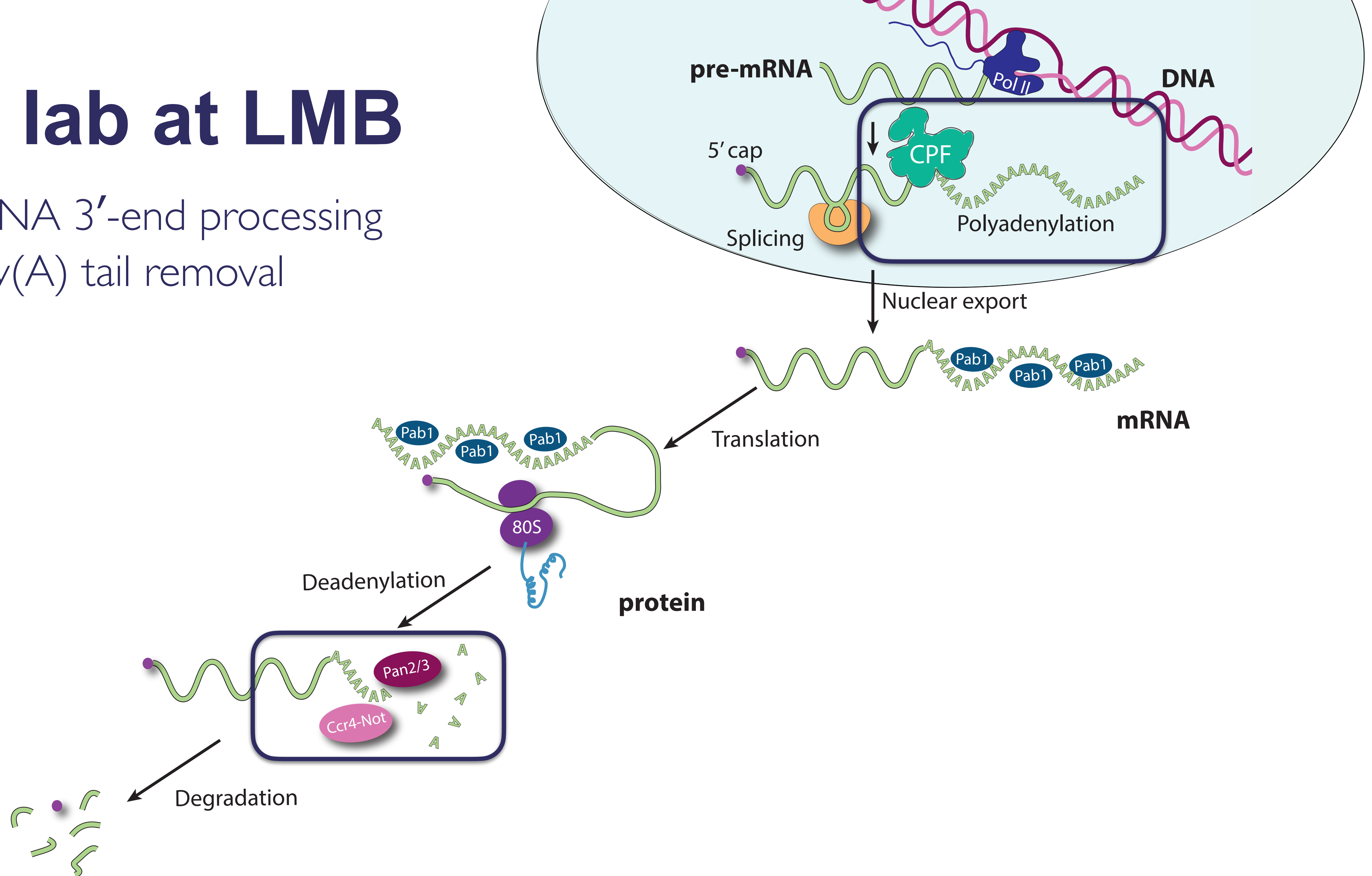
My lab at LMB

I. mRNA 3'-end processing



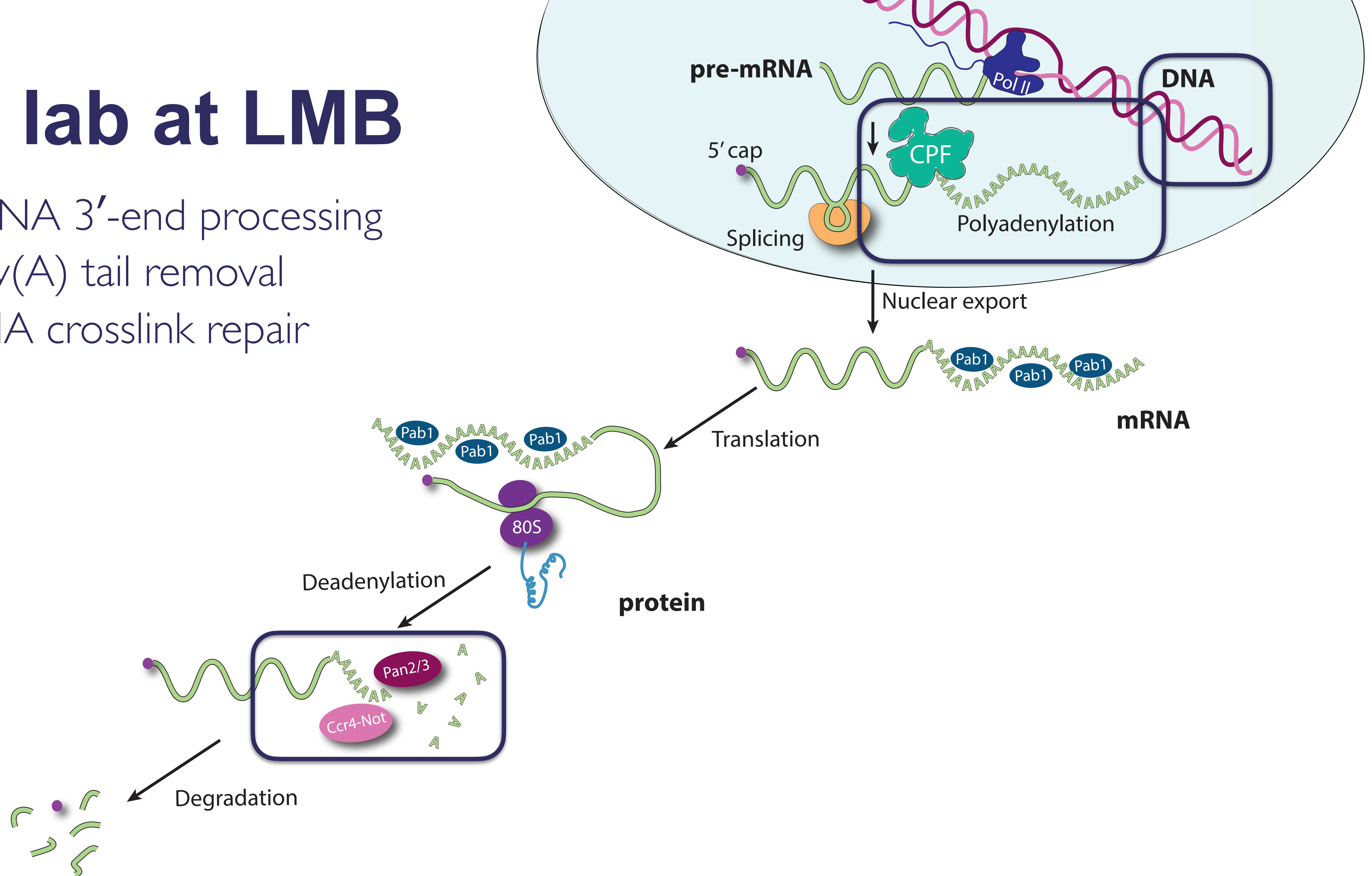
My lab at LMB

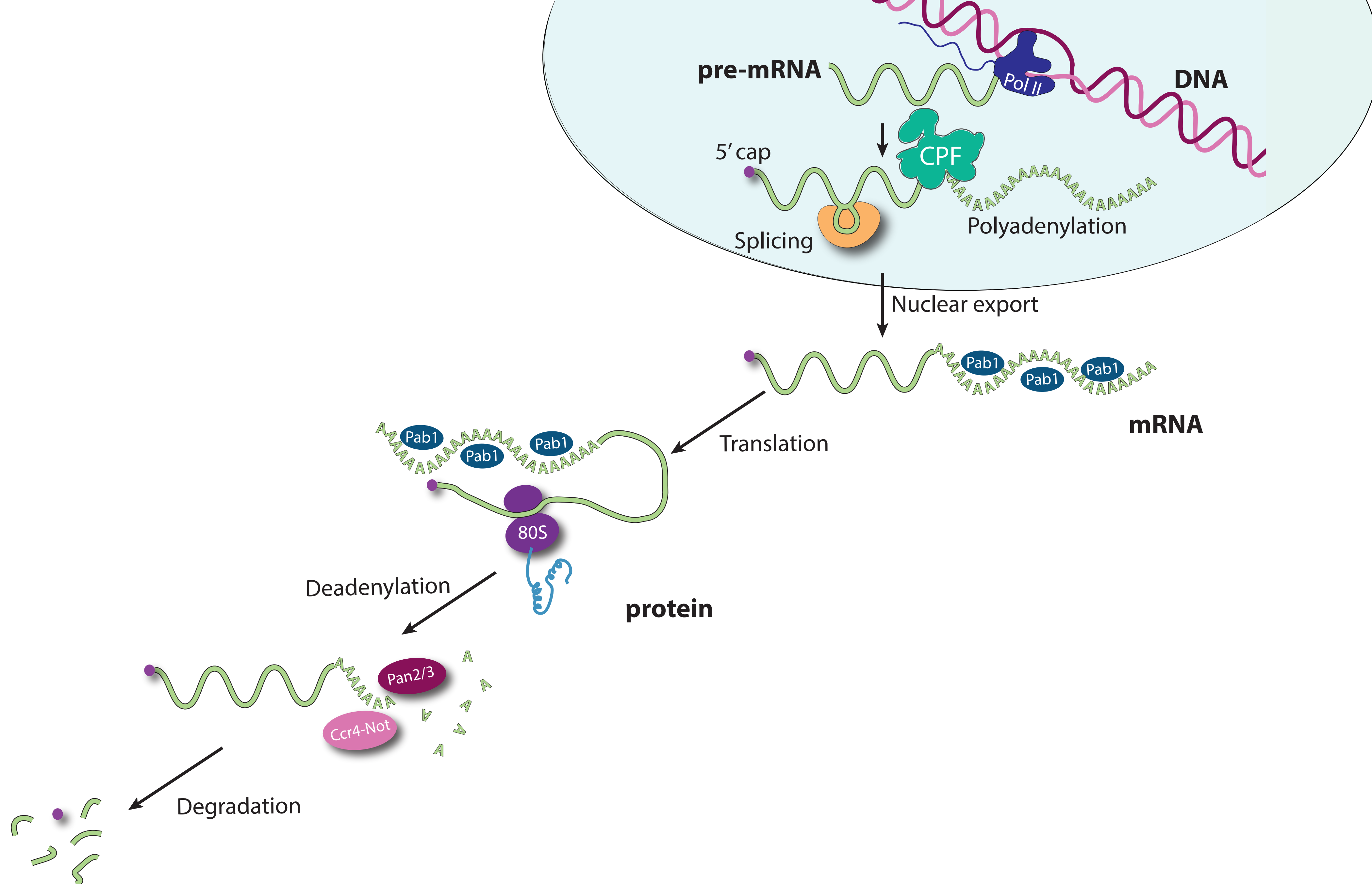
1. mRNA 3'-end processing
2. poly(A) tail removal

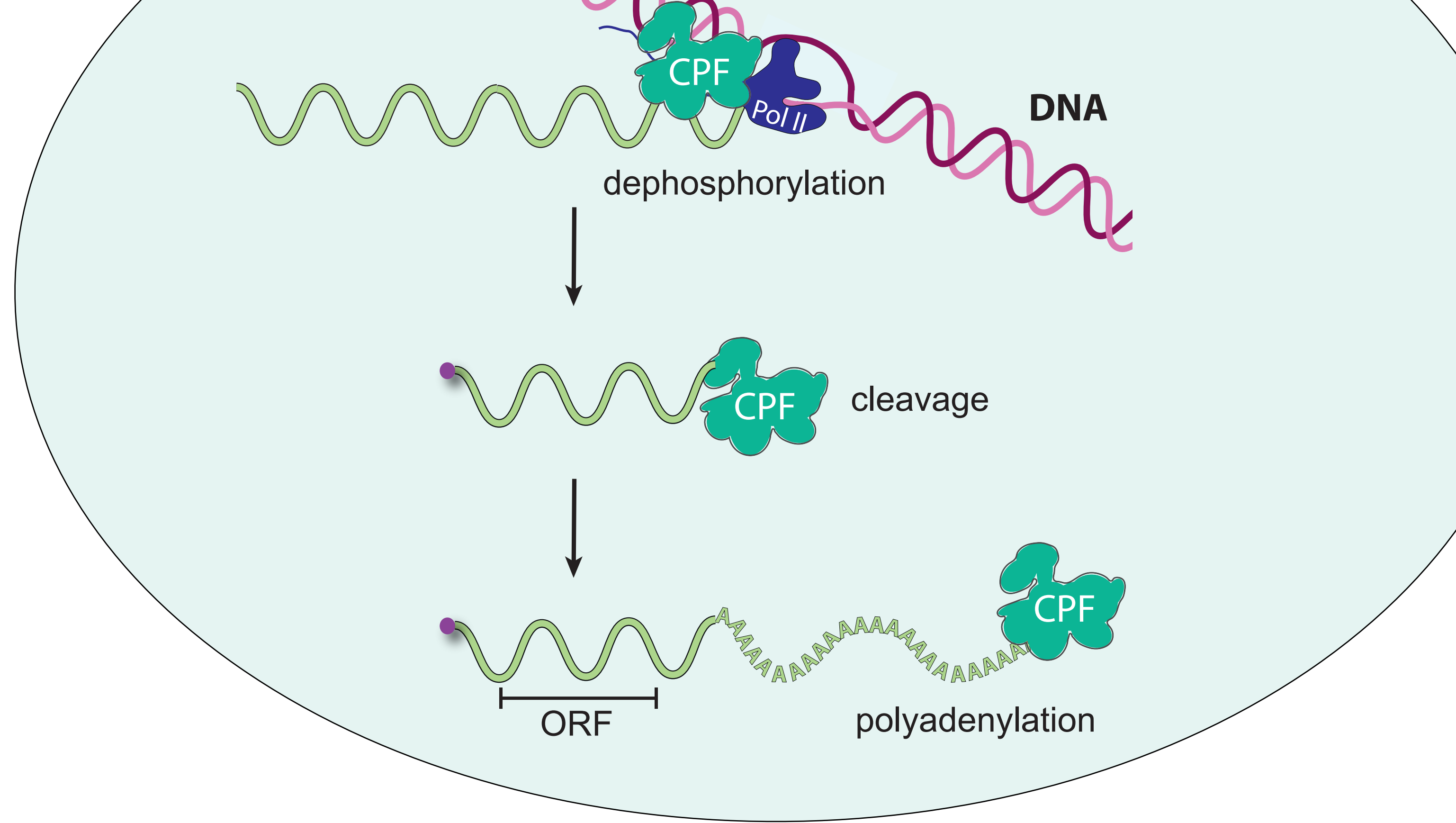
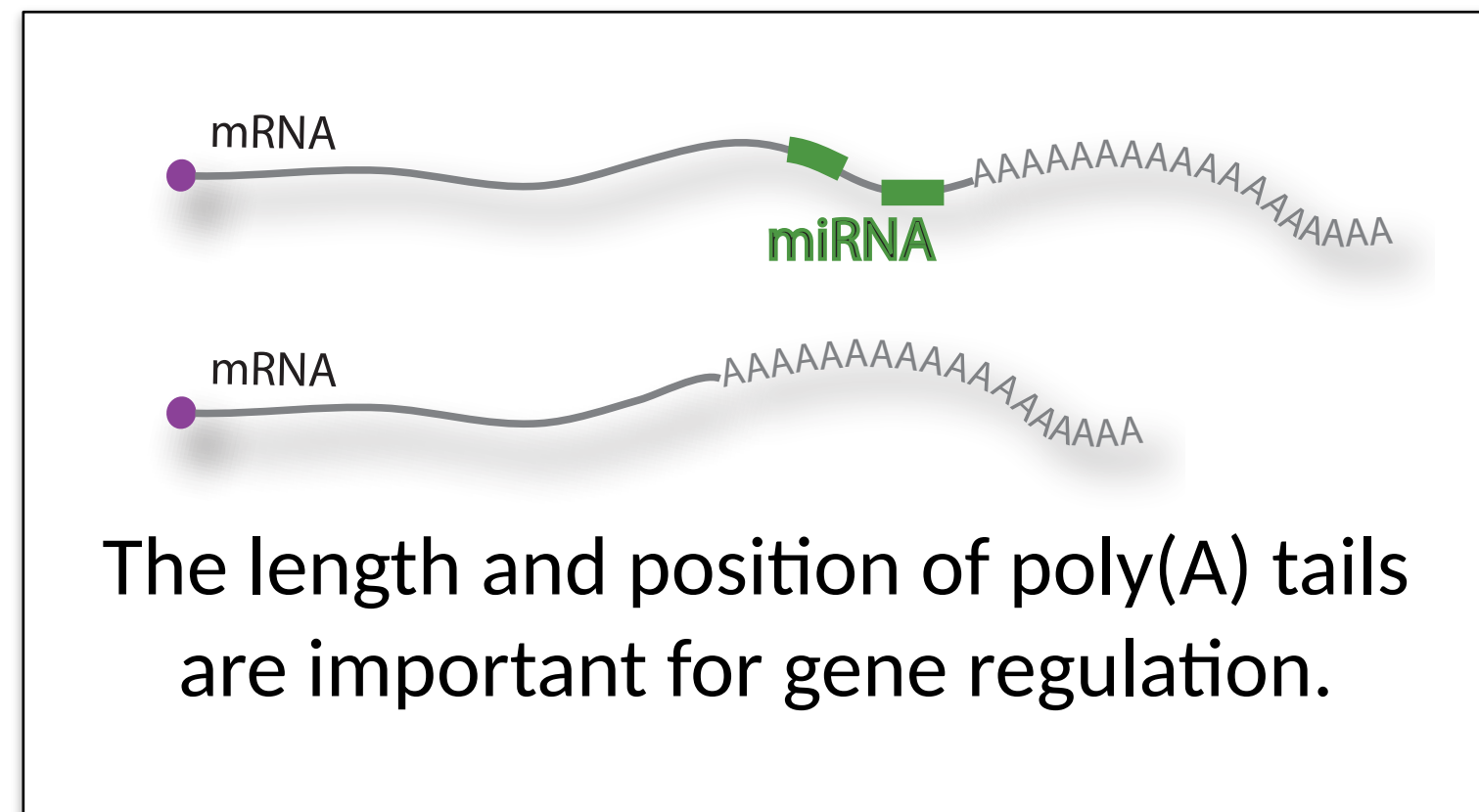


My lab at LMB

1. mRNA 3'-end processing
2. poly(A) tail removal
3. DNA crosslink repair





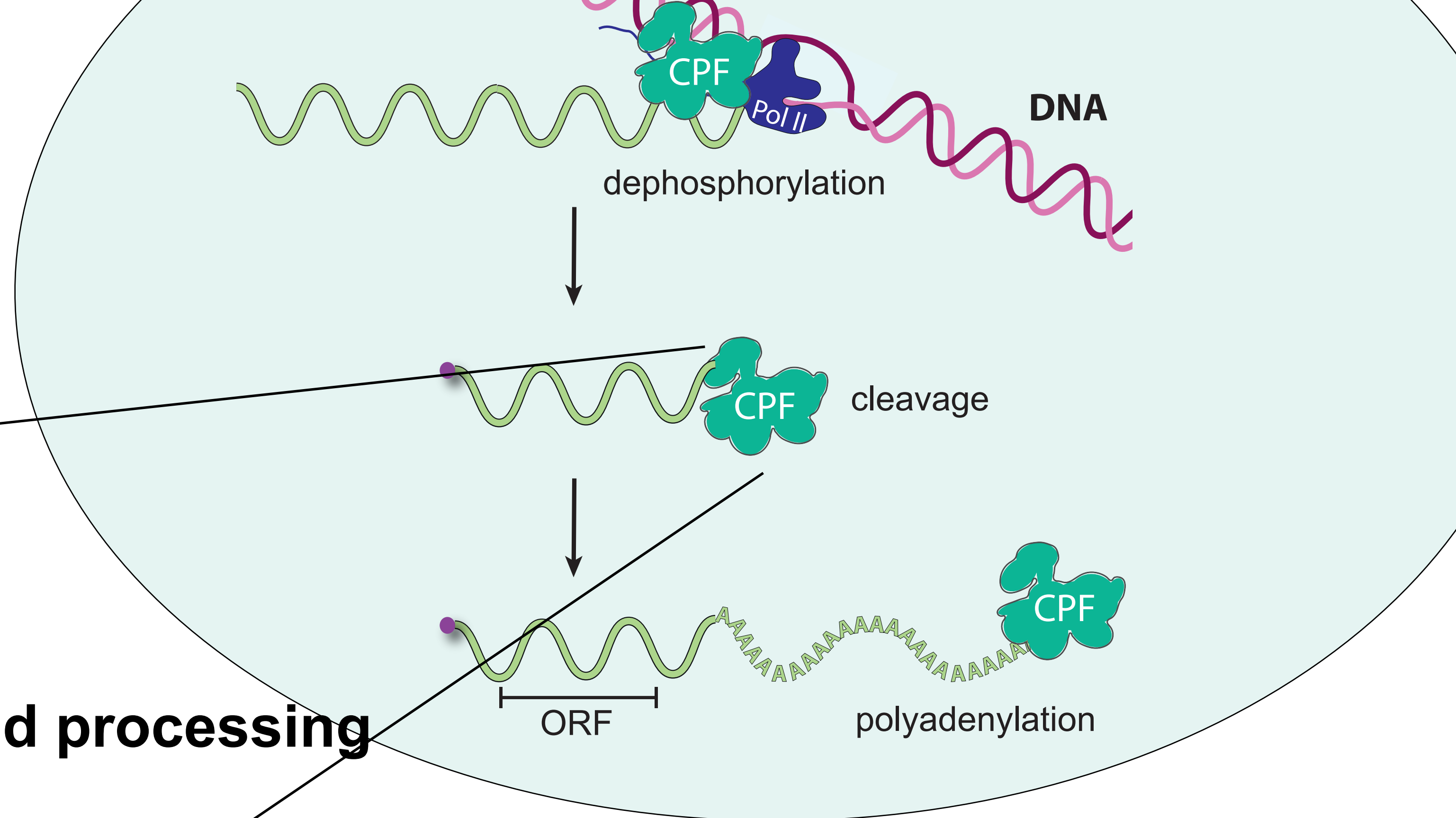


Globin mRNA polyA site mutations (LOF) - **thalassemia**

Prothrombin mRNA polyA site mutations (GOF) - **thrombophilia**

Alternative polyadenylation - **cancer**

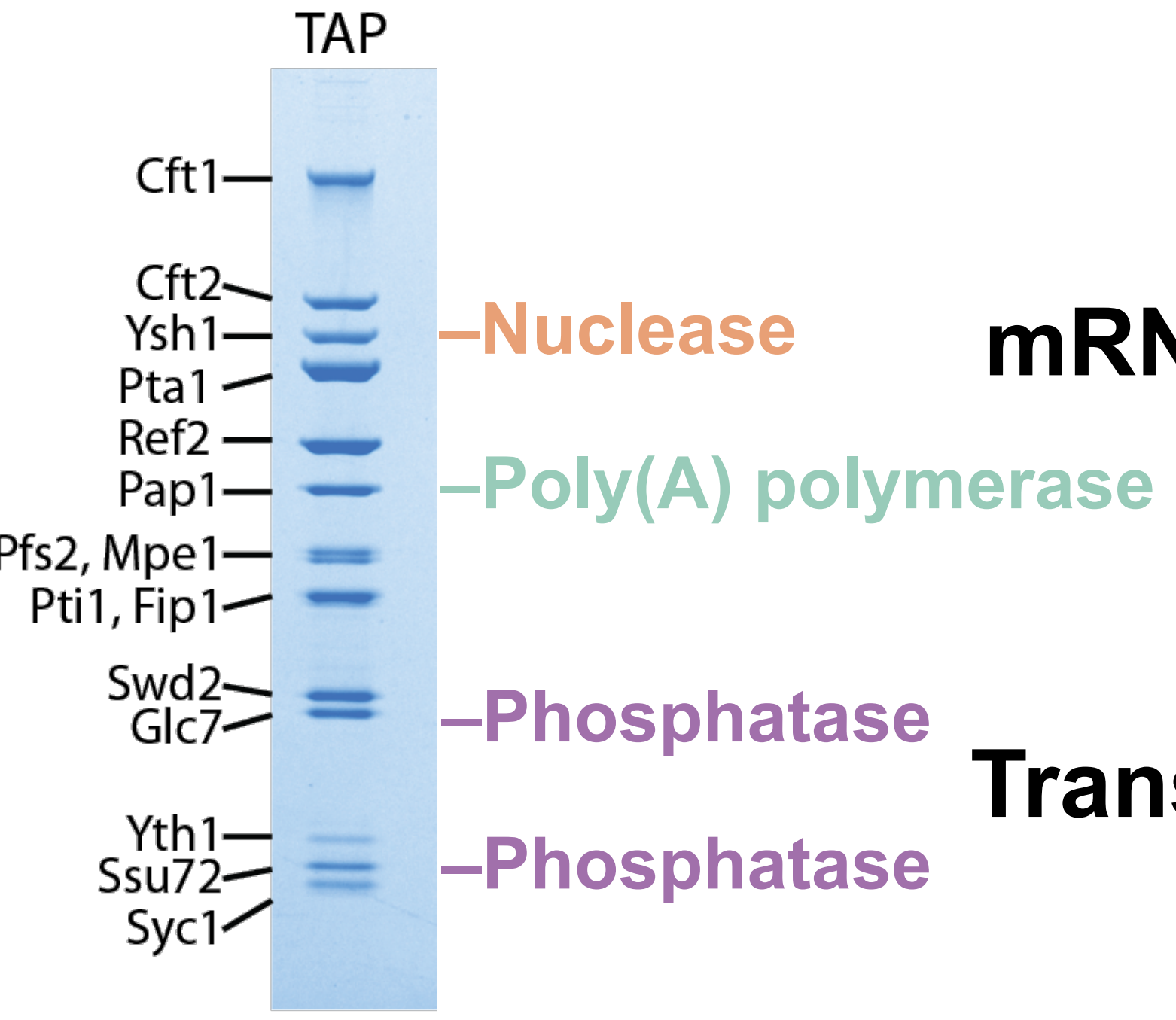
Disruption of host polyadenylation - **influenza A**



mRNA 3' end processing

Transcription termination

+



Nuclease

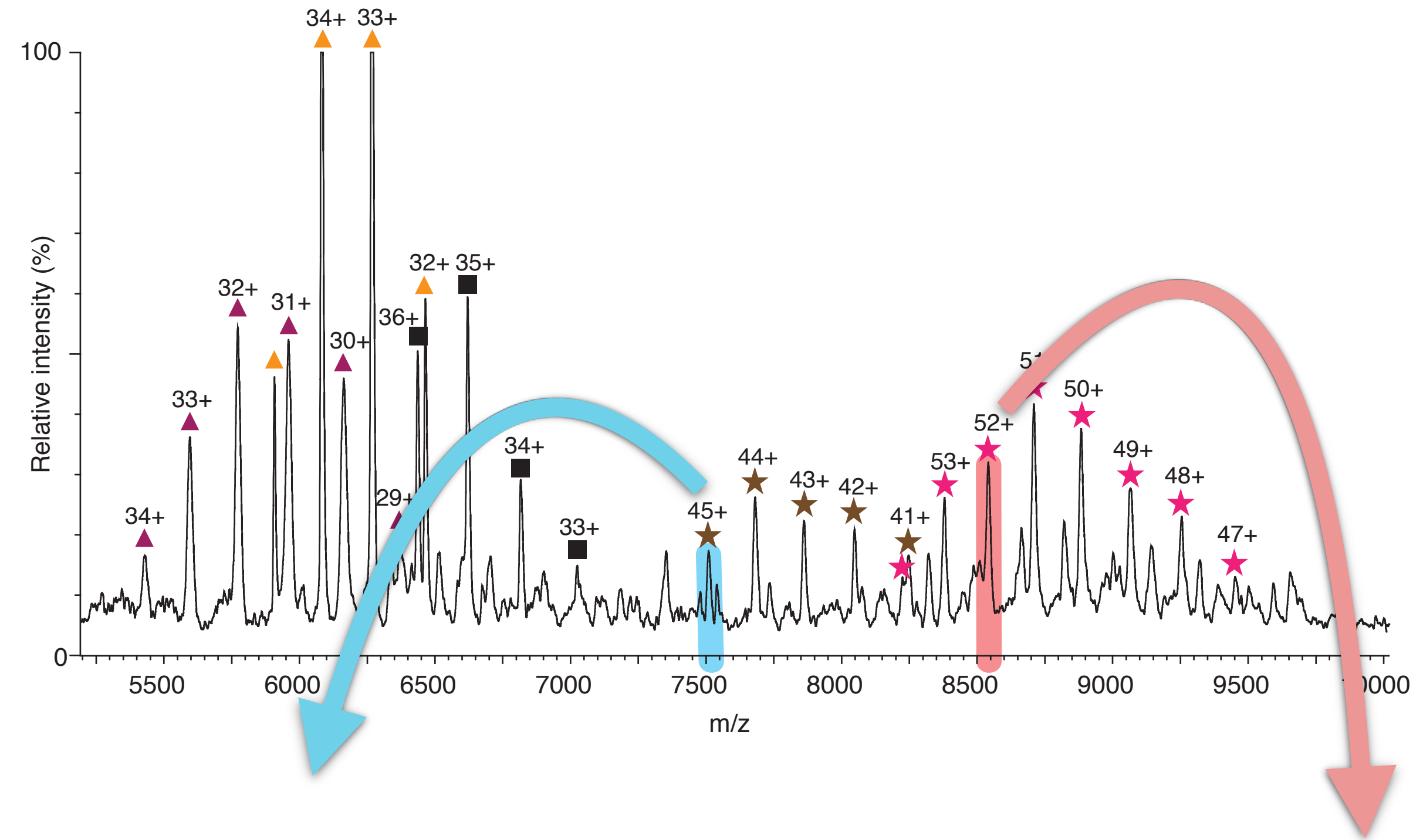
Poly(A) polymerase

Phosphatase

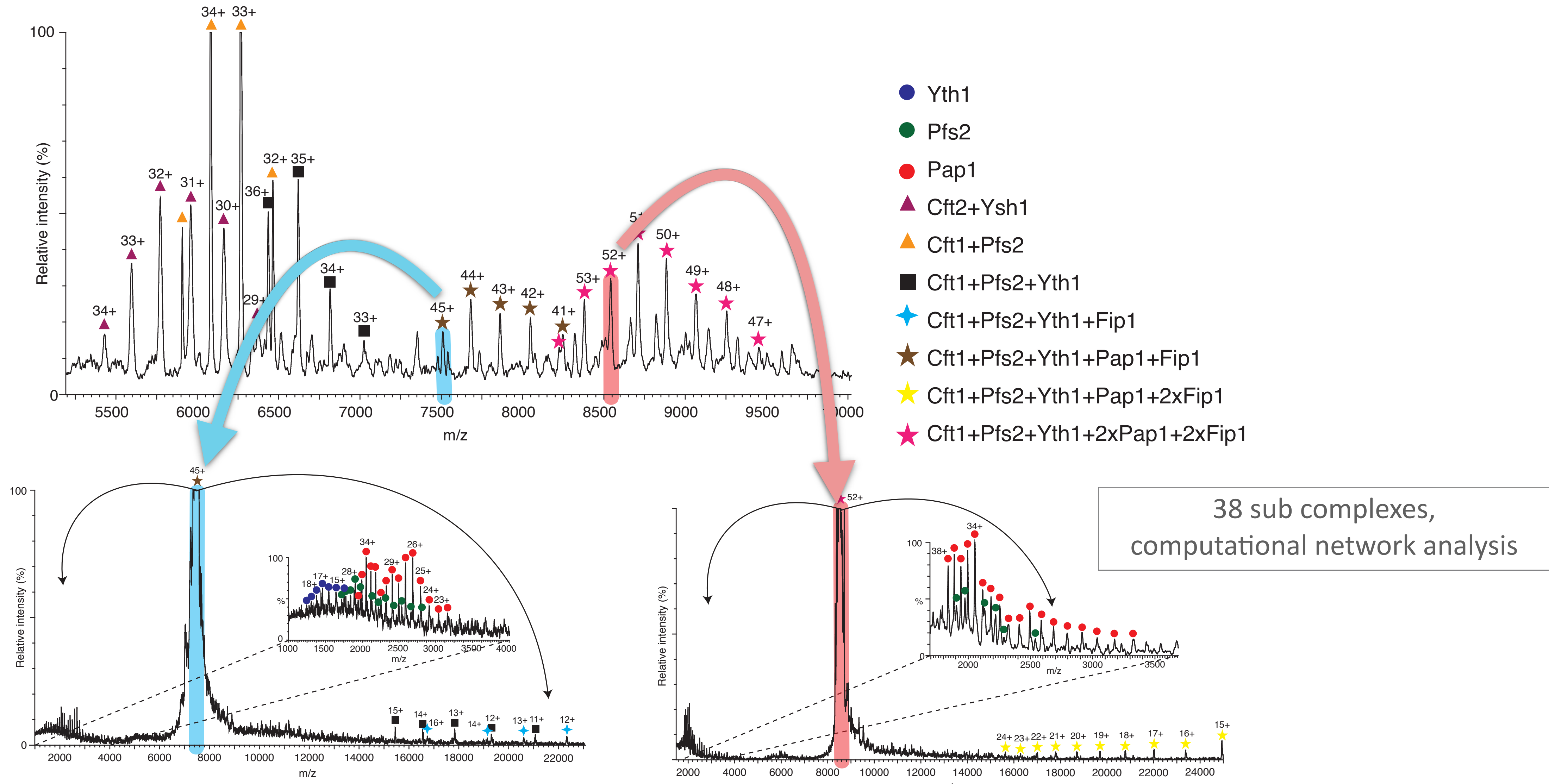
Phosphatase

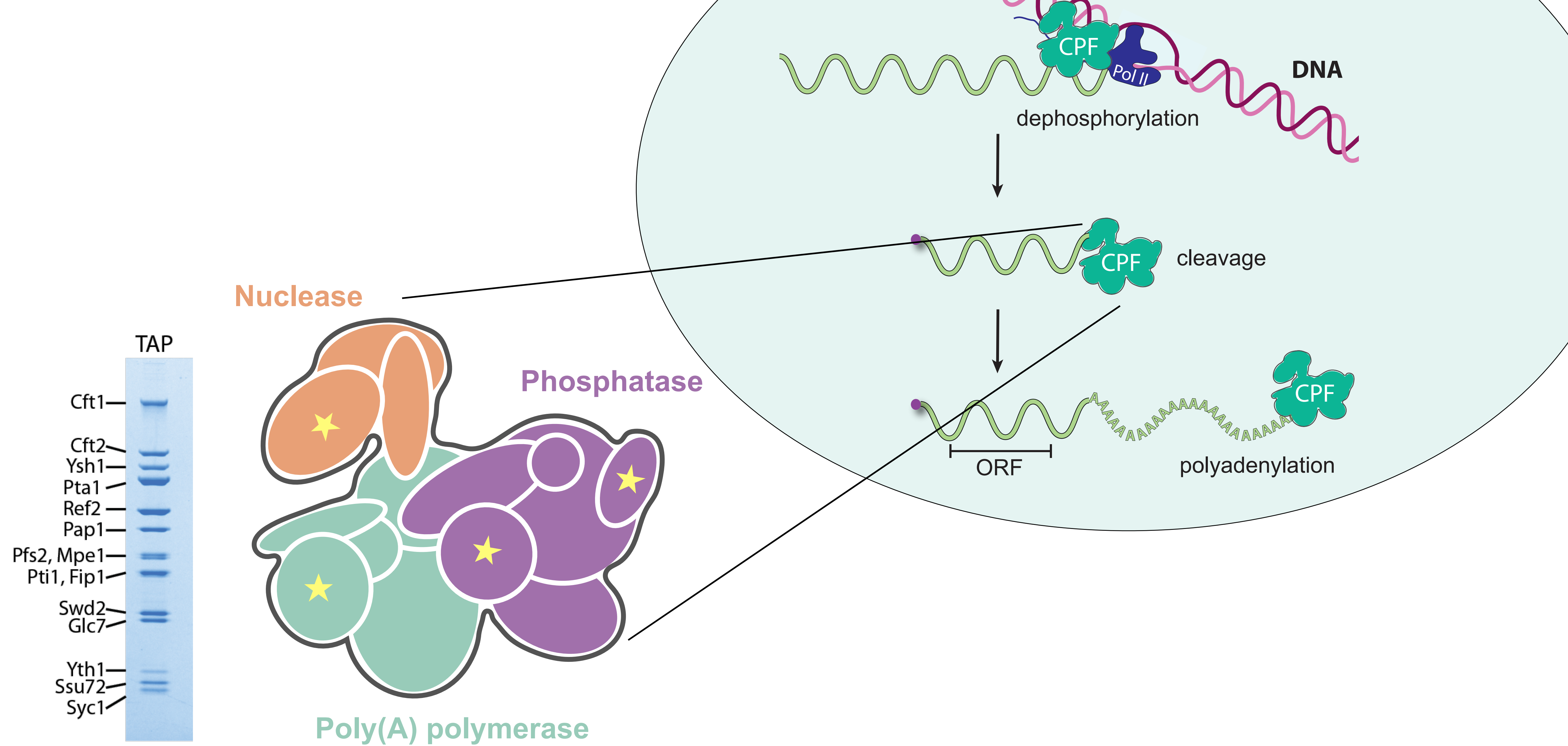
Identification of enzymatic modules in CPF

Identification of enzymatic modules in CPF

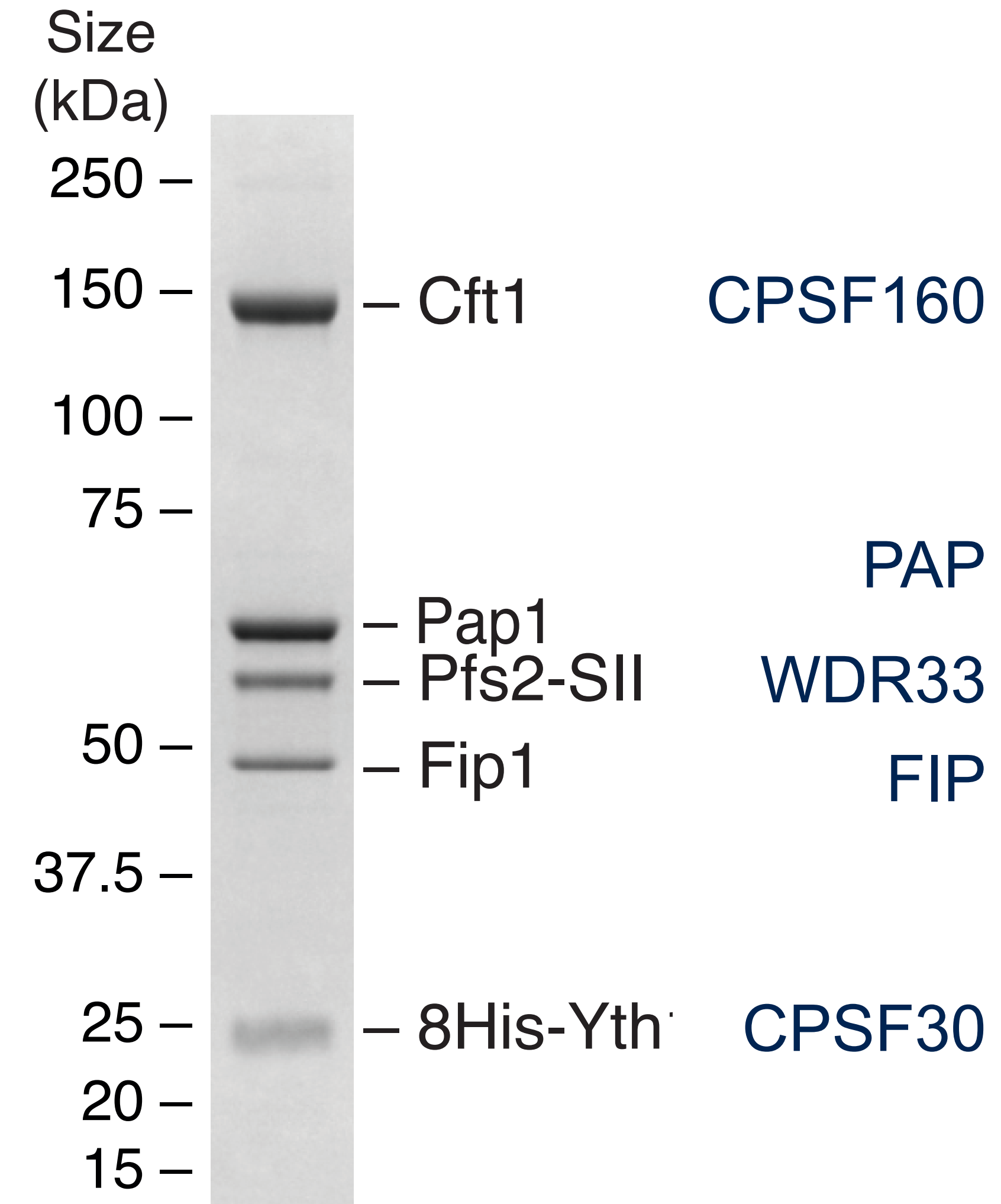
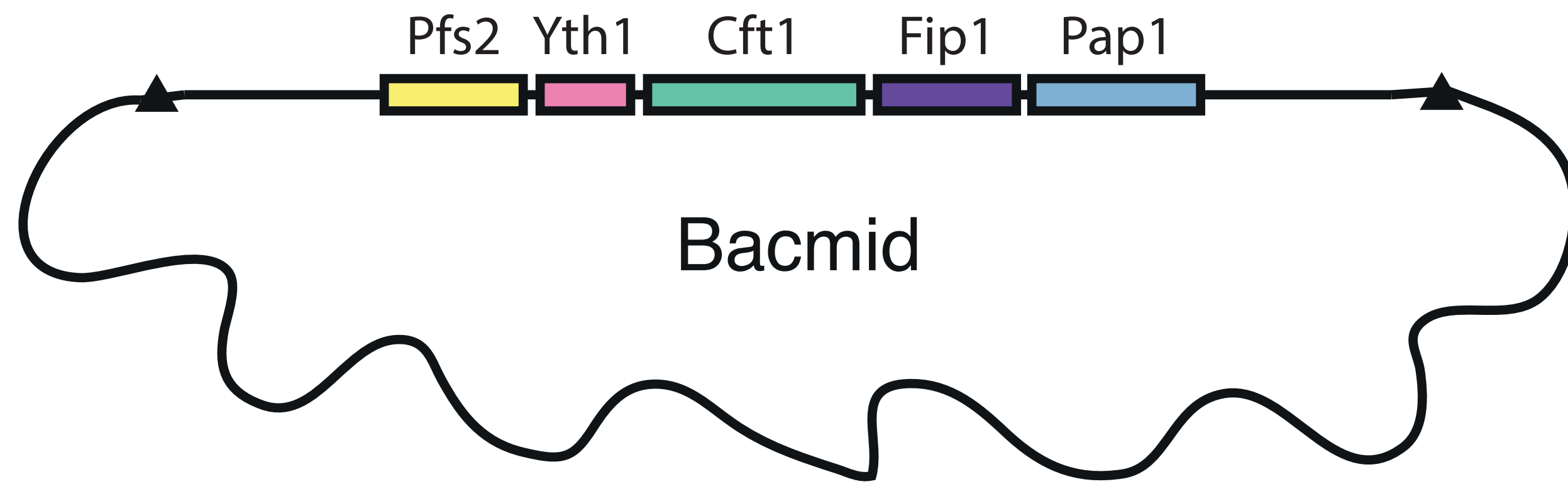


Identification of enzymatic modules in CPF



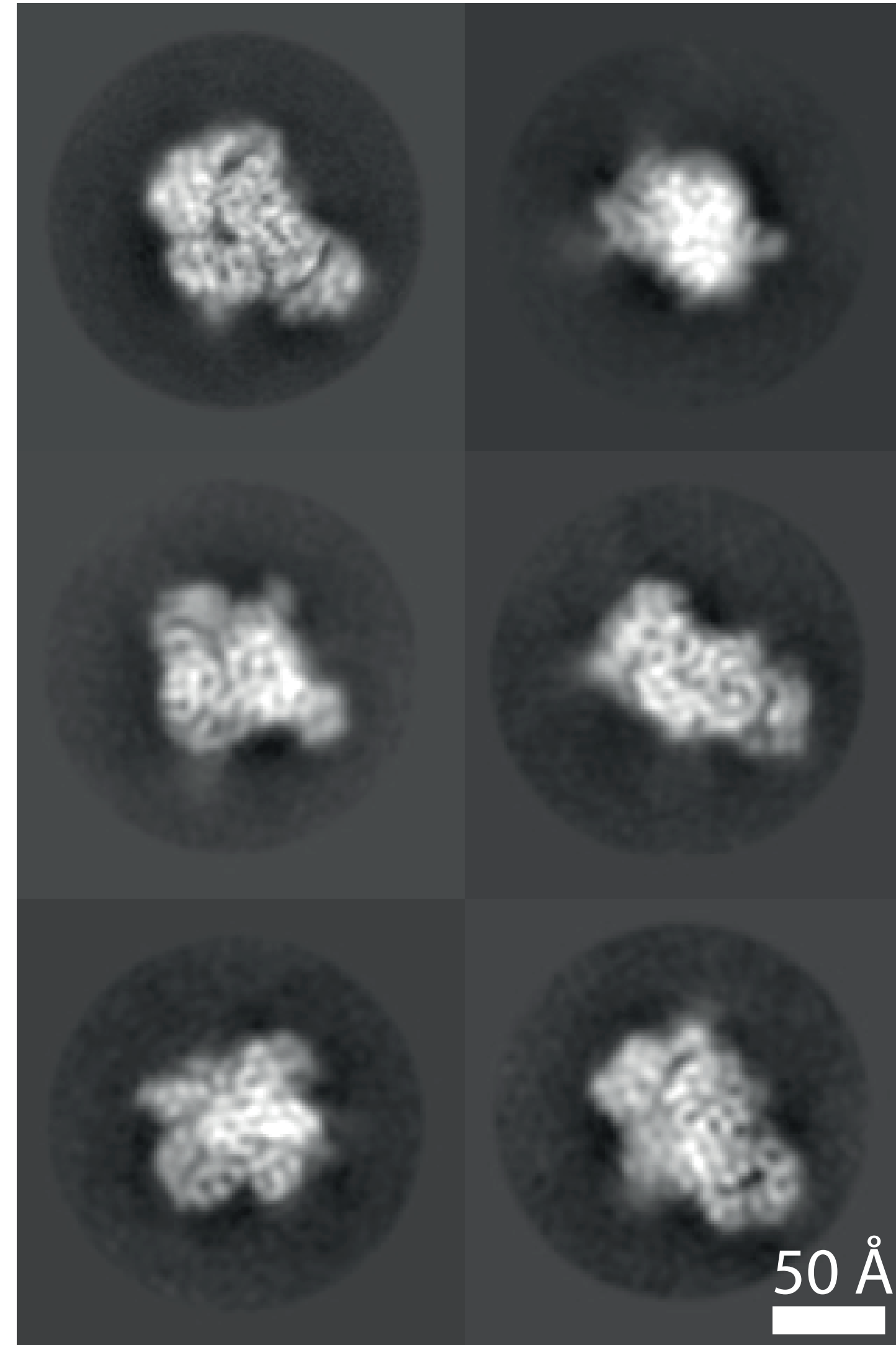
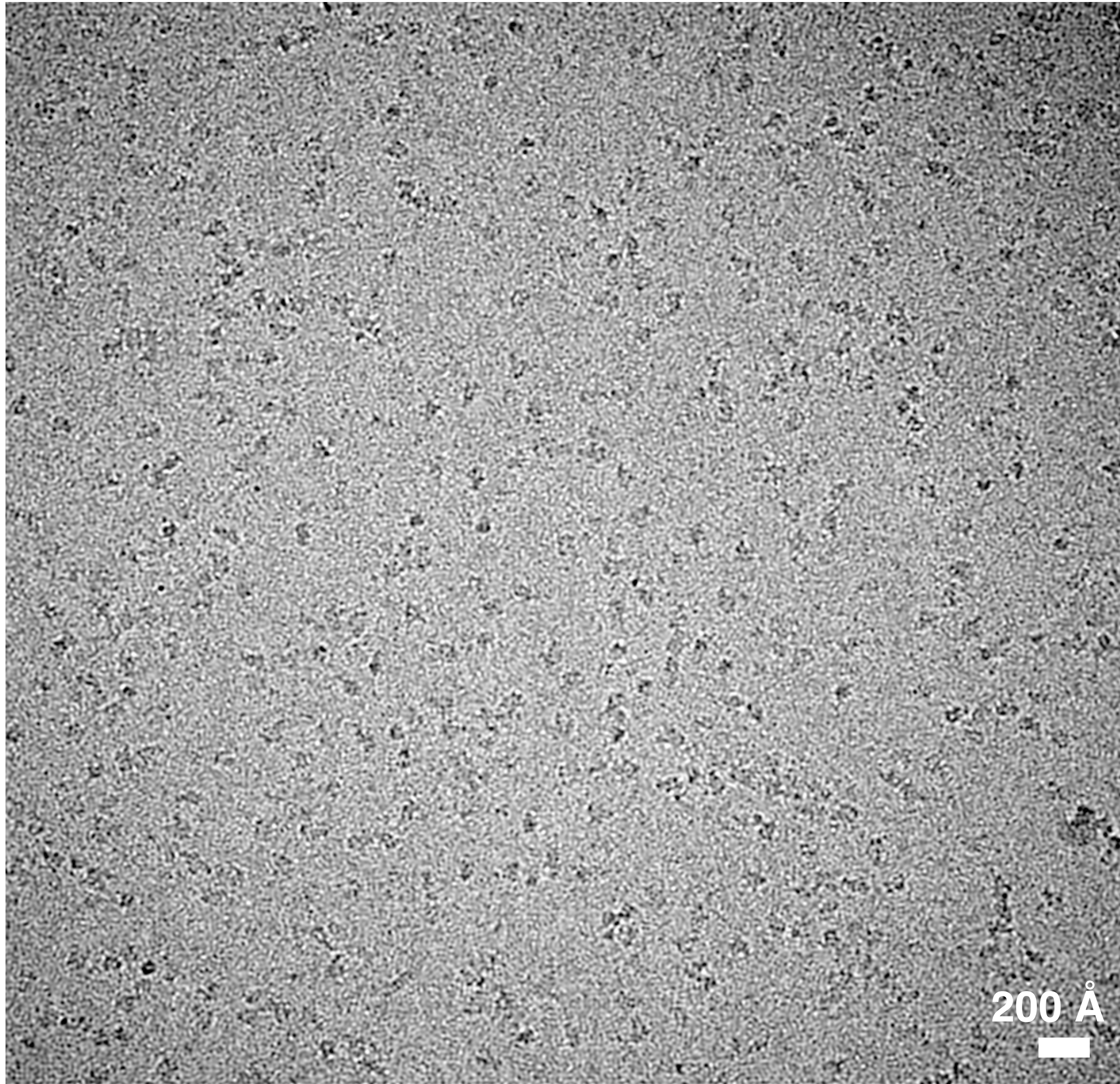


The polymerase module



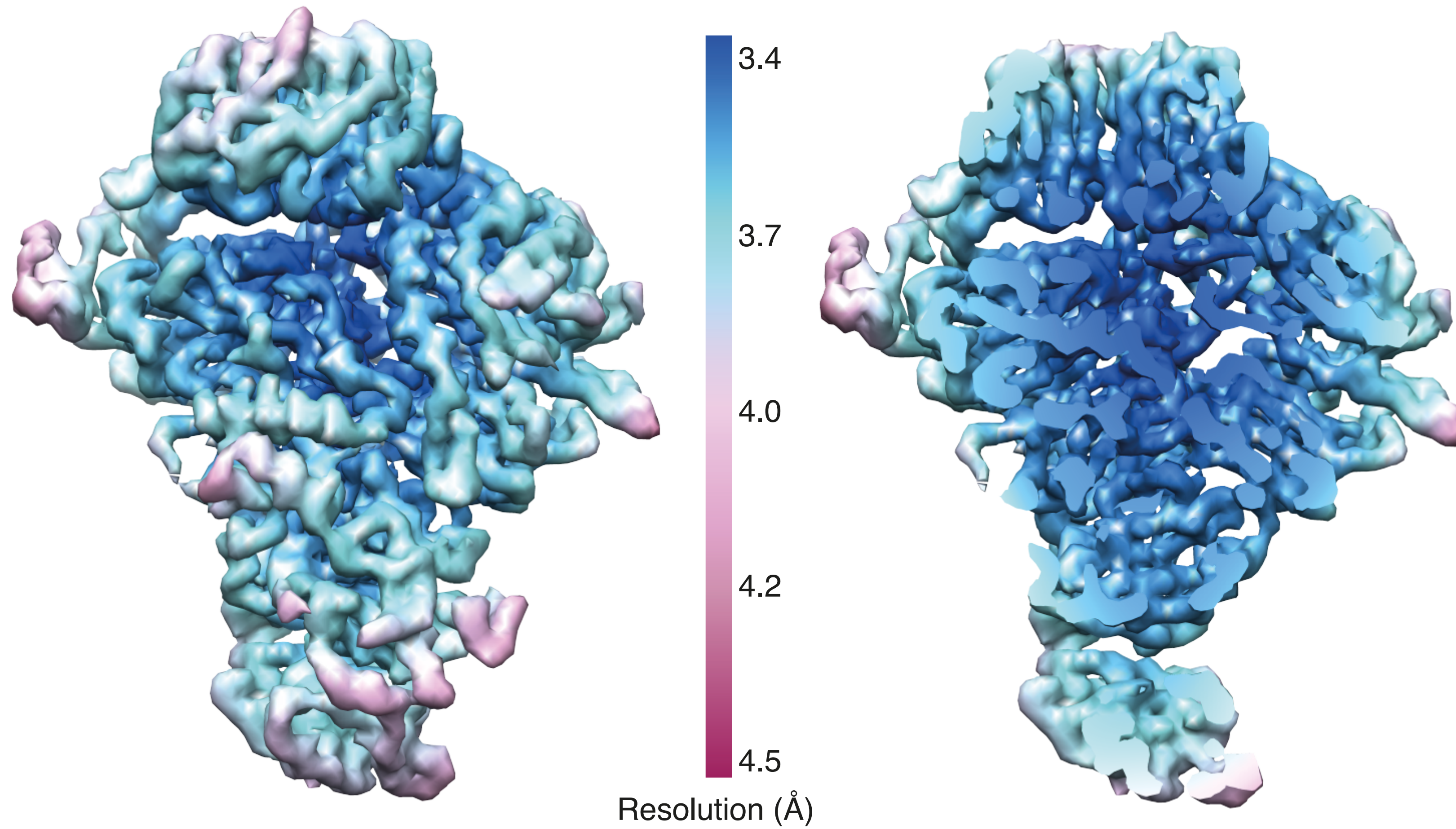
Ananth Kumar
Ana Casañal

The polymerase module



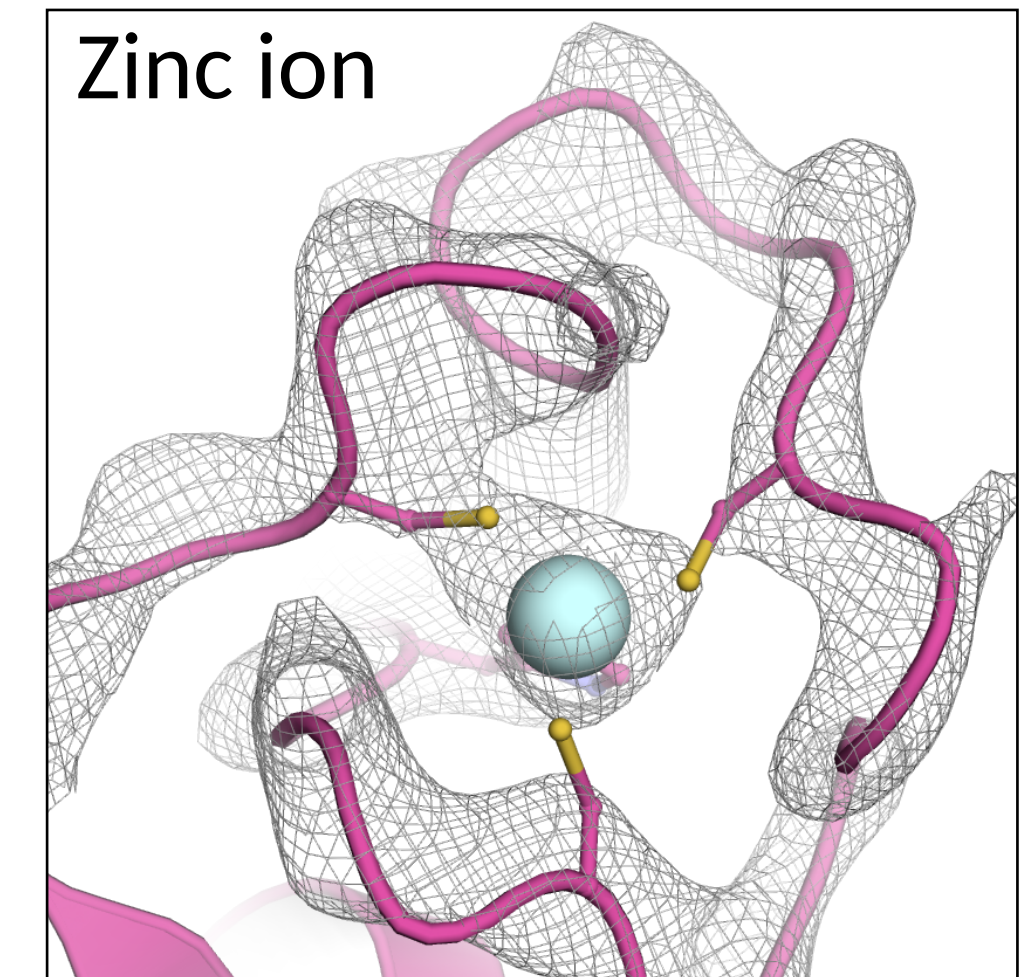
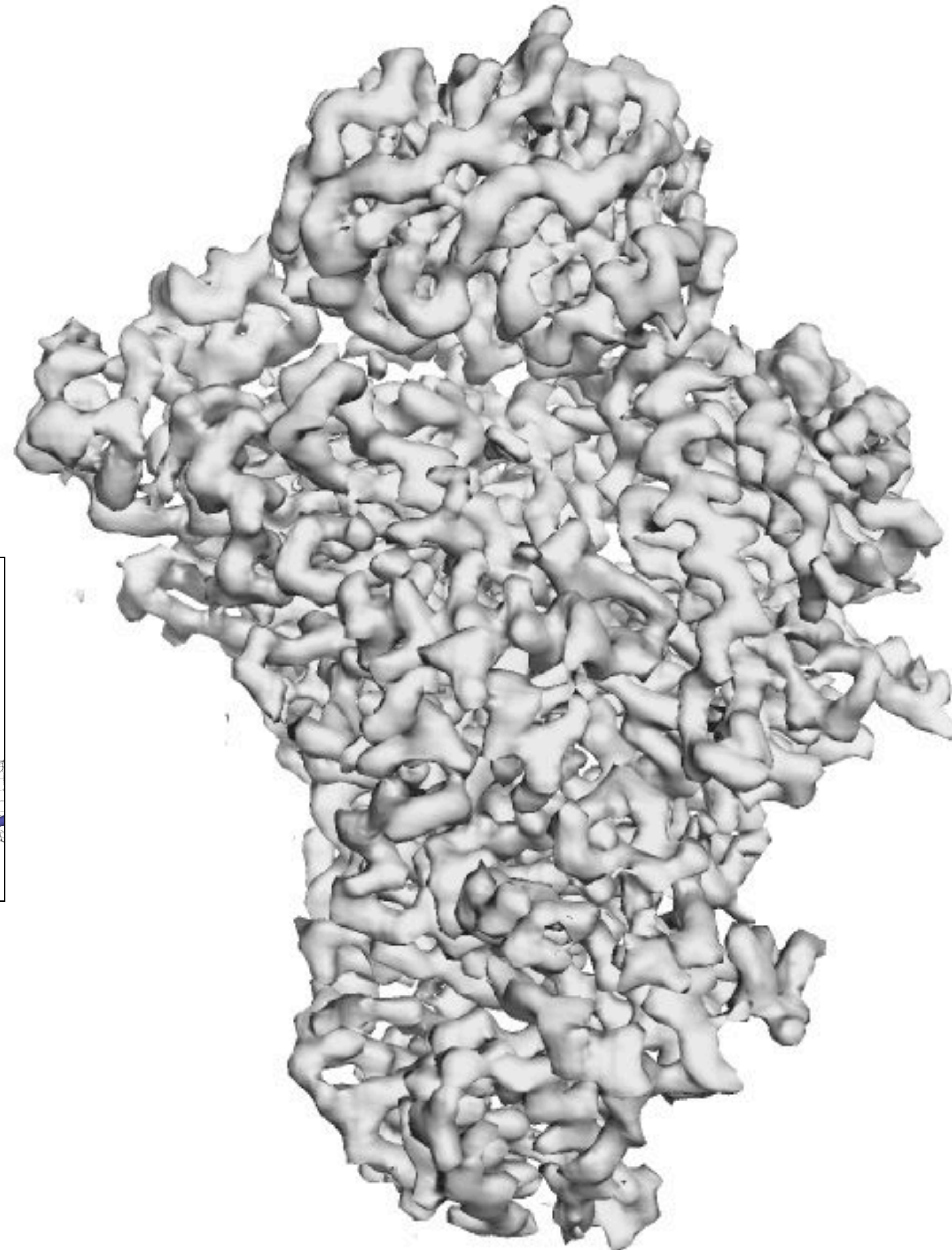
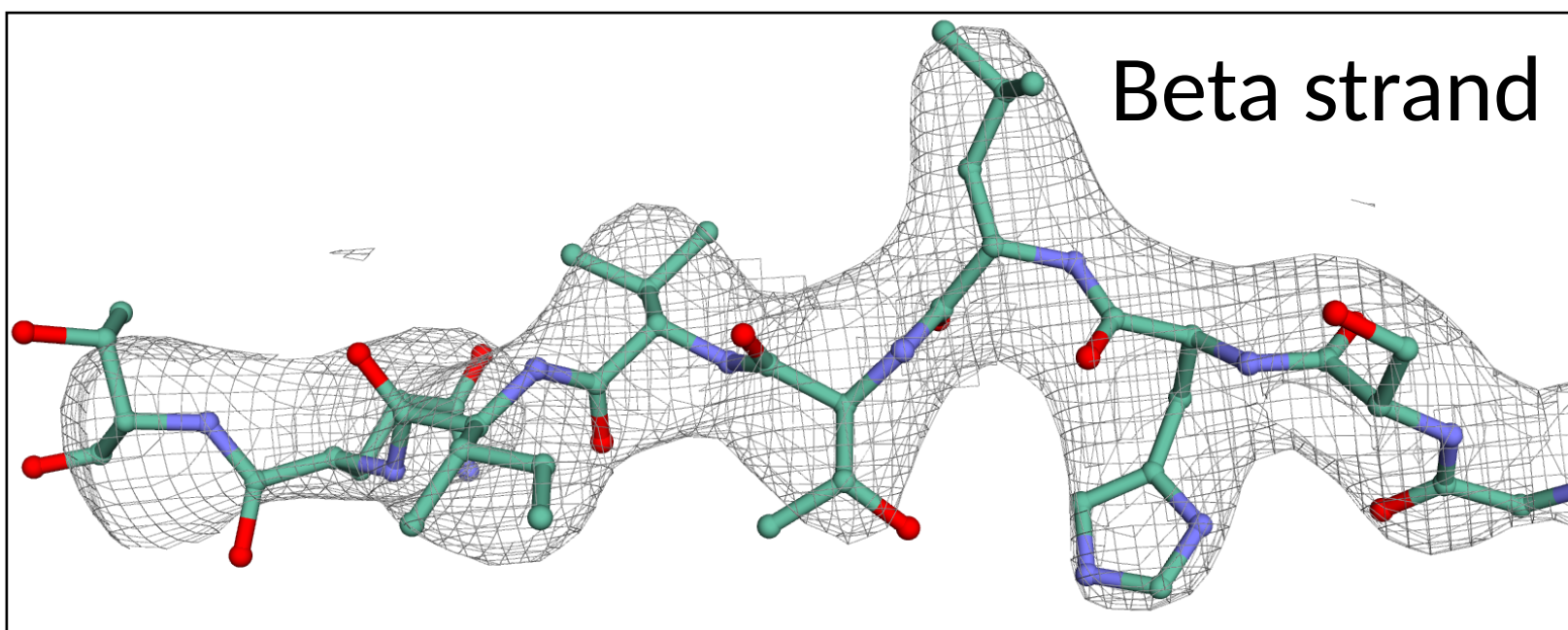
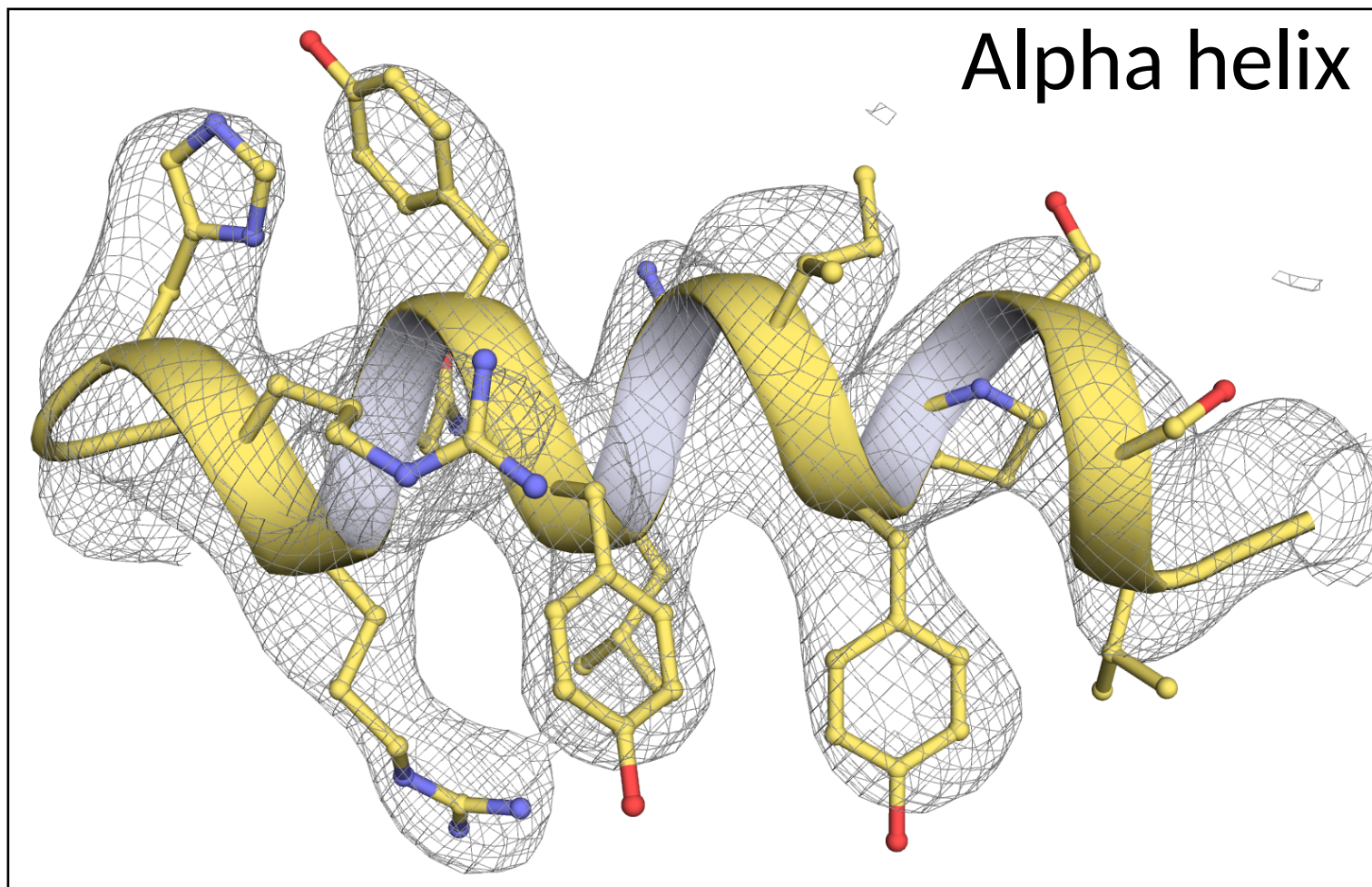
~ 200 kDa
No polymerase

Cryo-EM of the polymerase module



Relion 2
79,950 particles

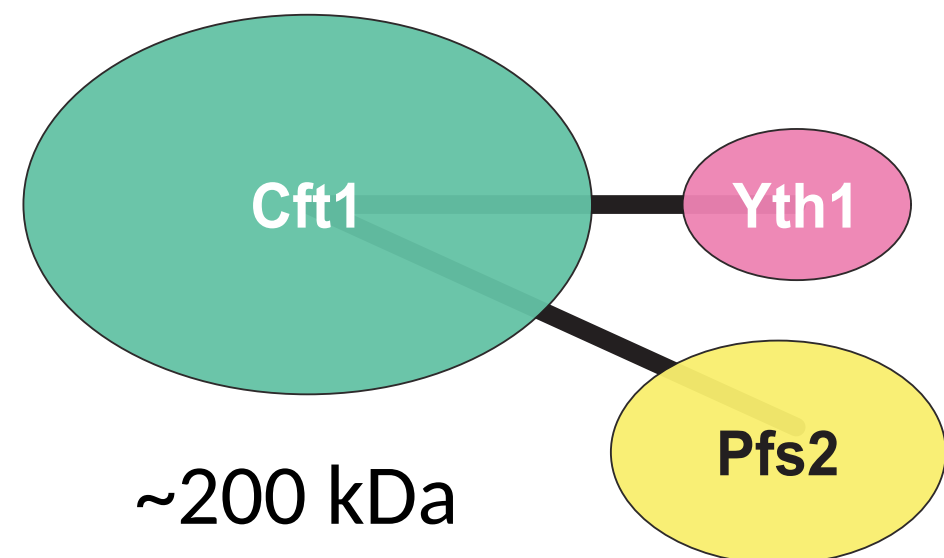
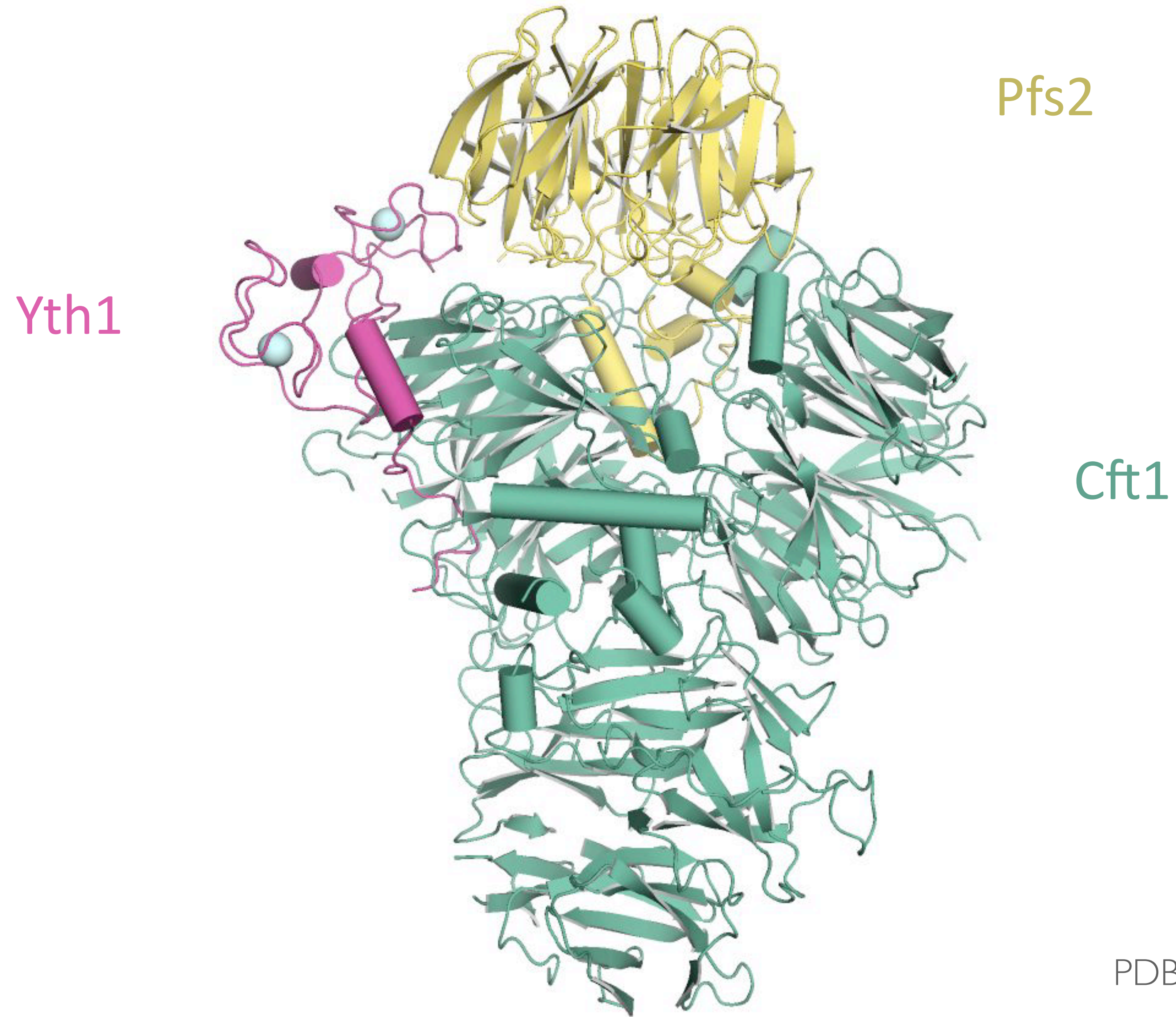
The polymerase module



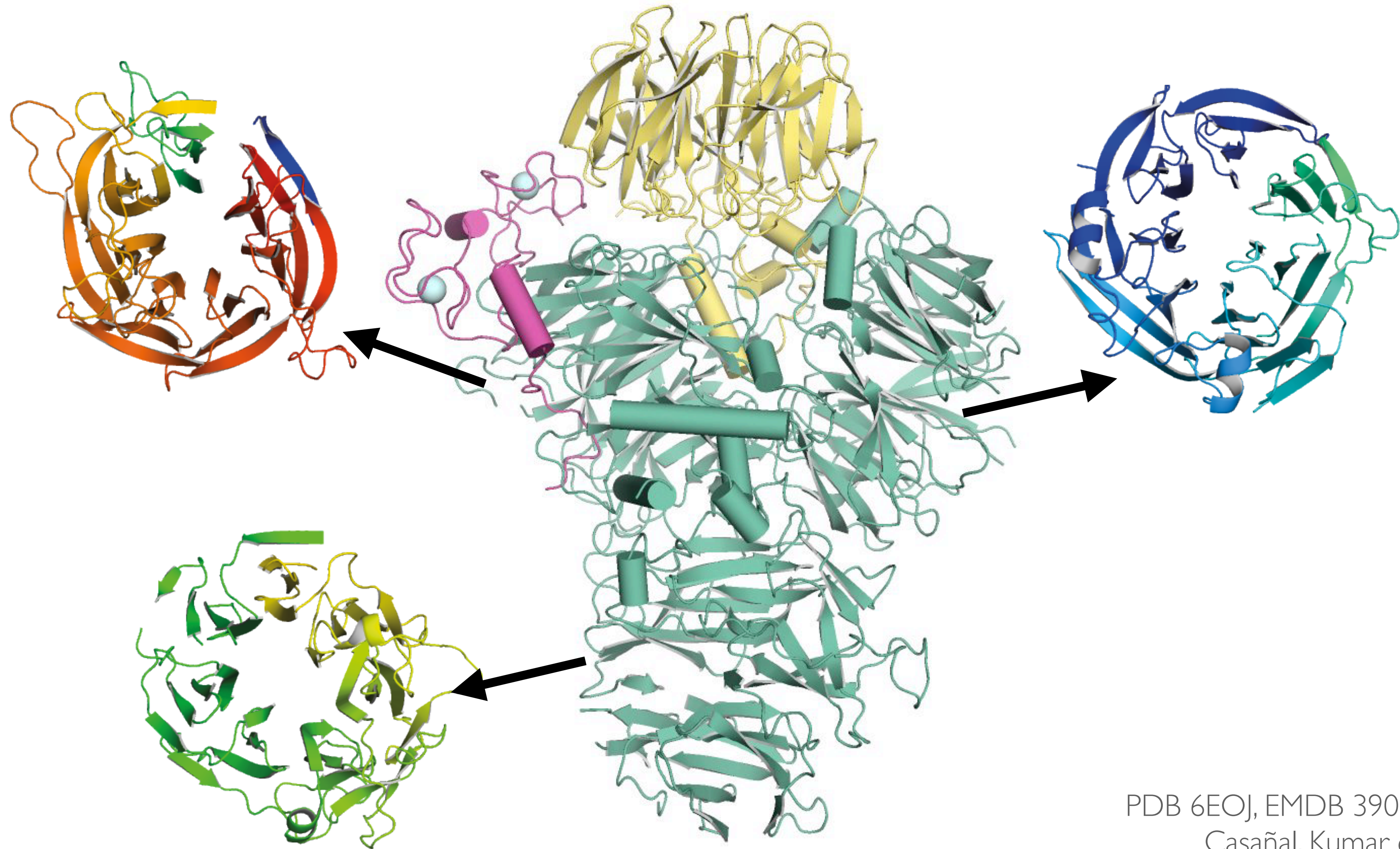
Ananth Kumar
Ana Casañal

- 3.5 Å resolution overall
- 3D classification
- focussed classification for individual domains with heterogeneity/flexibility

The polymerase module



The polymerase module

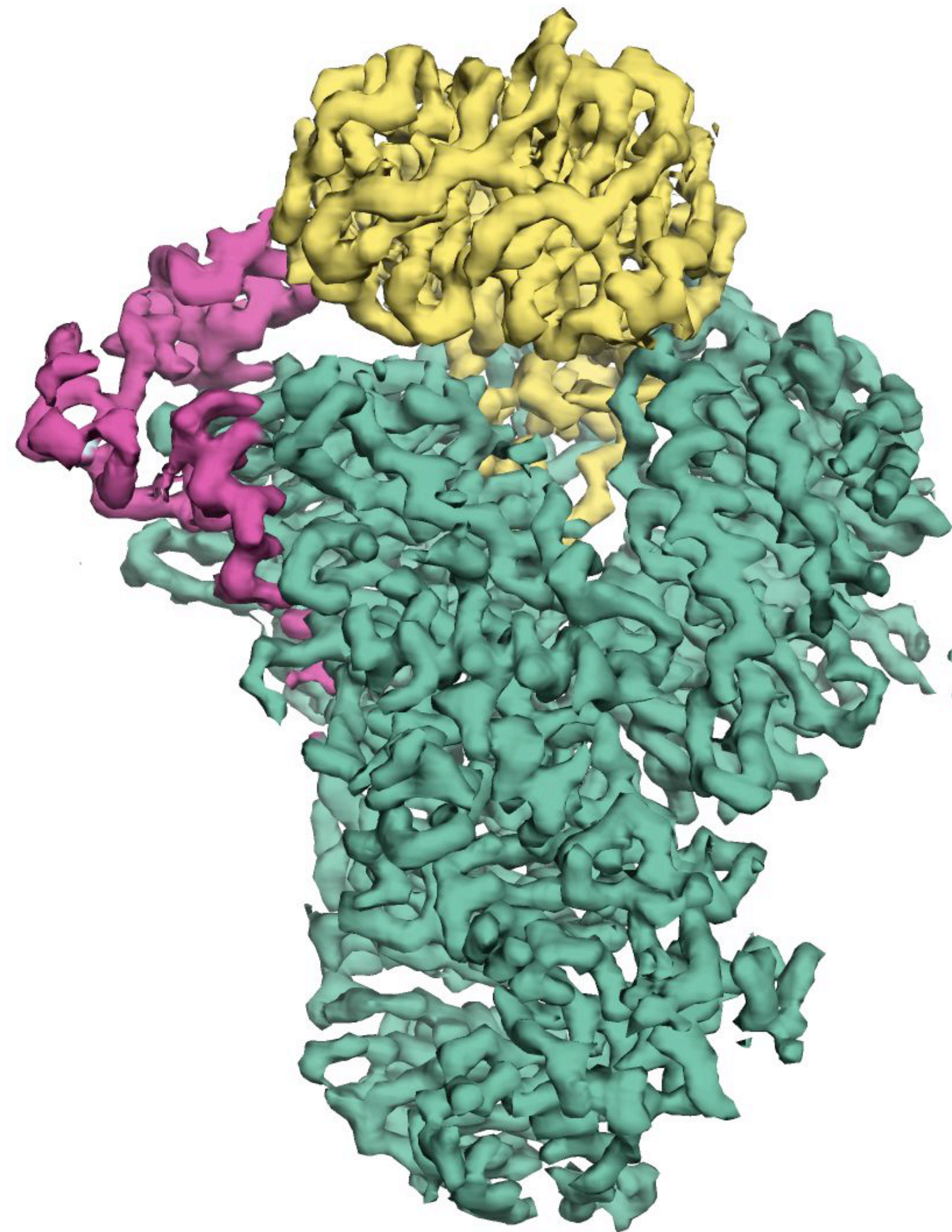


PDB 6EOJ, EMDB 3908, EMPIAR 10299
Casañal, Kumar *et al* Science 2017

Interaction of YthI with the polymerase module

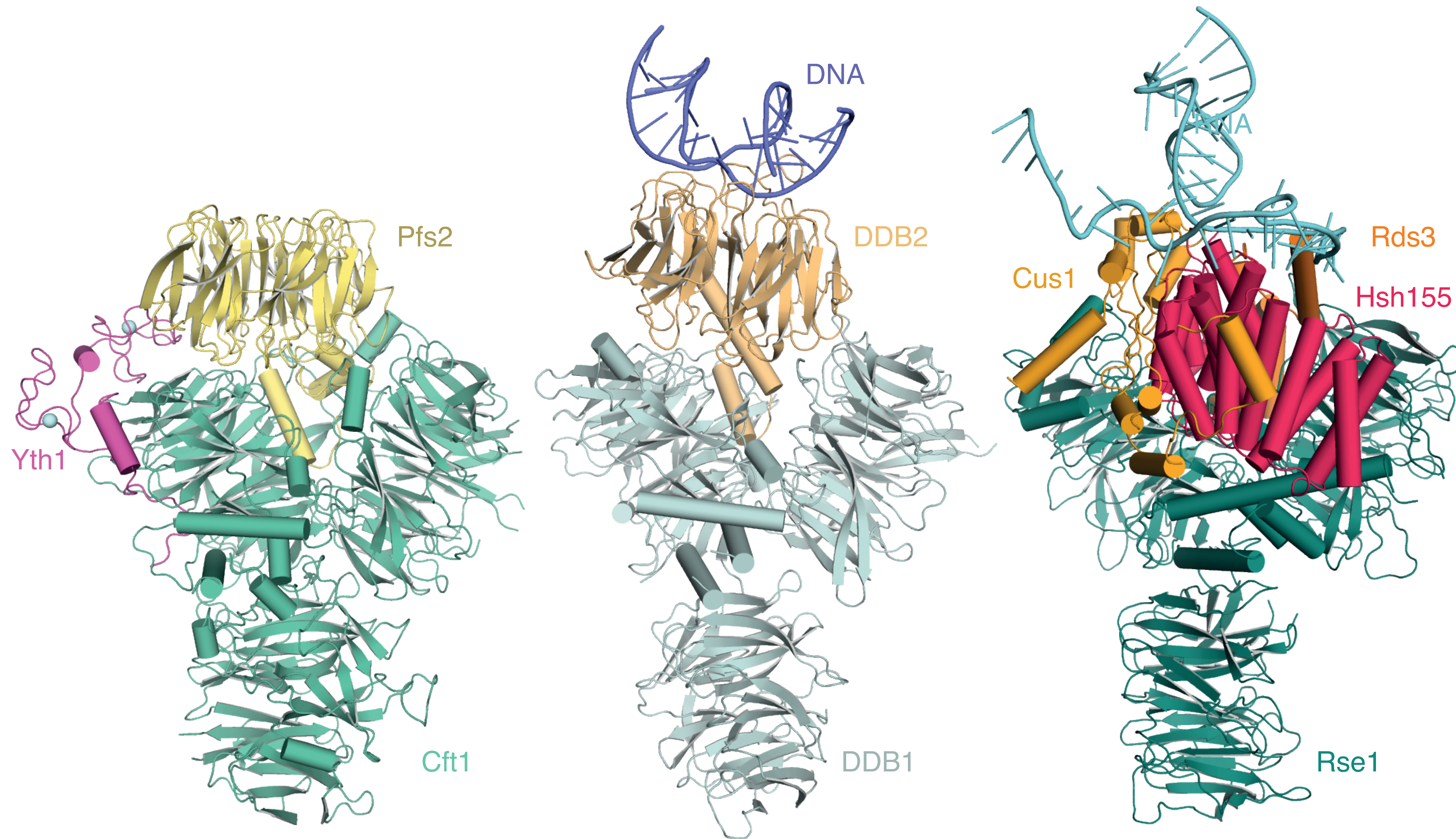


Interaction of Pfs2 with polymerase module



PDB 6EOJ, EMDB 3908, EMPIAR 10299
Casañal, Kumar *et al* *Science* 2017

Similarity to other nucleic acid binding complexes



mRNA 3' end processing
CPF polymerase module

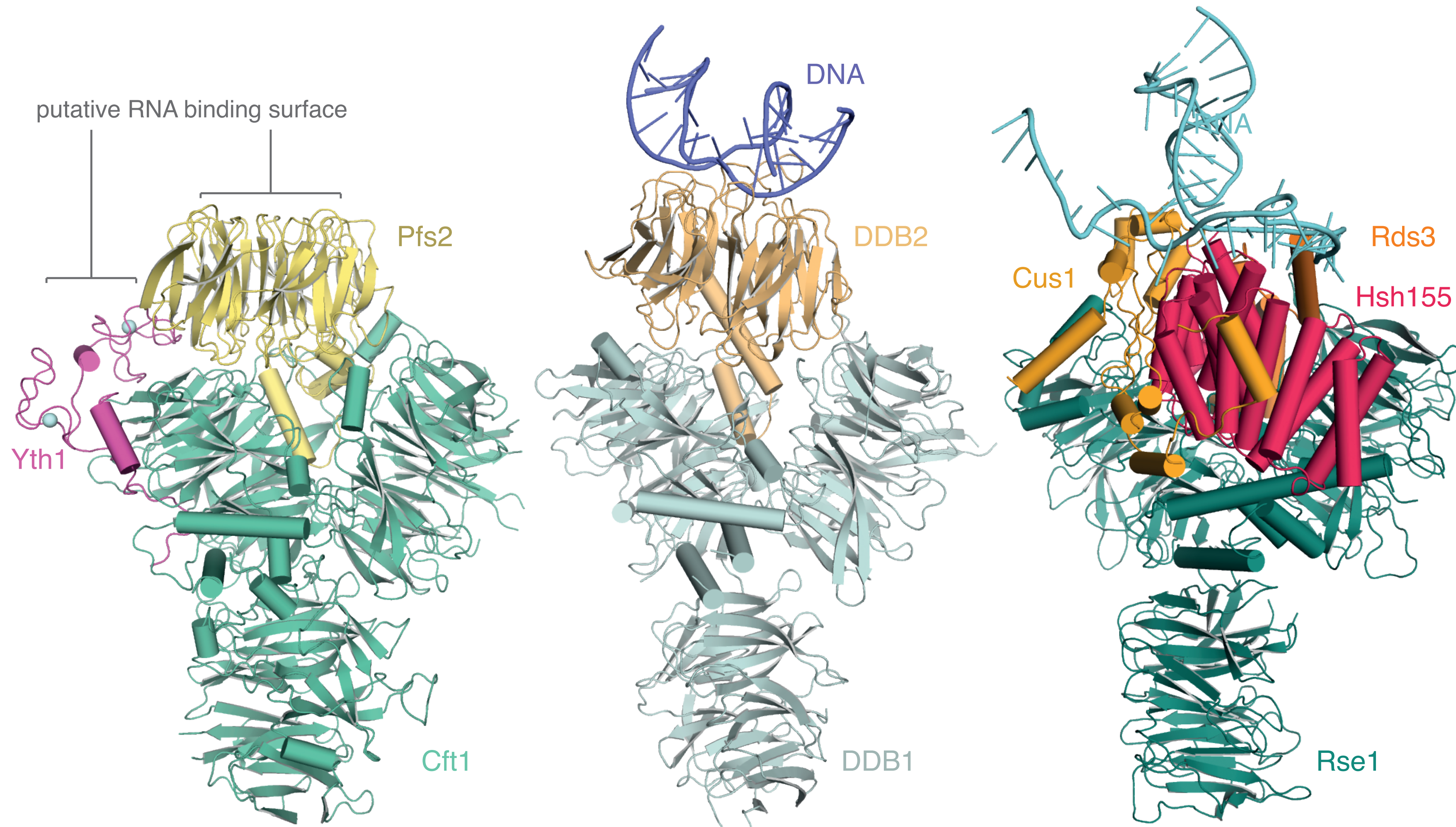
DNA repair
DDB1-DDB2

pre-mRNA splicing
SF3b

Scrima et al (2008)

Yan et al (2016)
Cretu et al (2016)
Plaschka et al (2017)

Similarity to other nucleic acid binding complexes



mRNA 3' end processing
CPF polymerase module

DNA repair
DDB1-DDB2

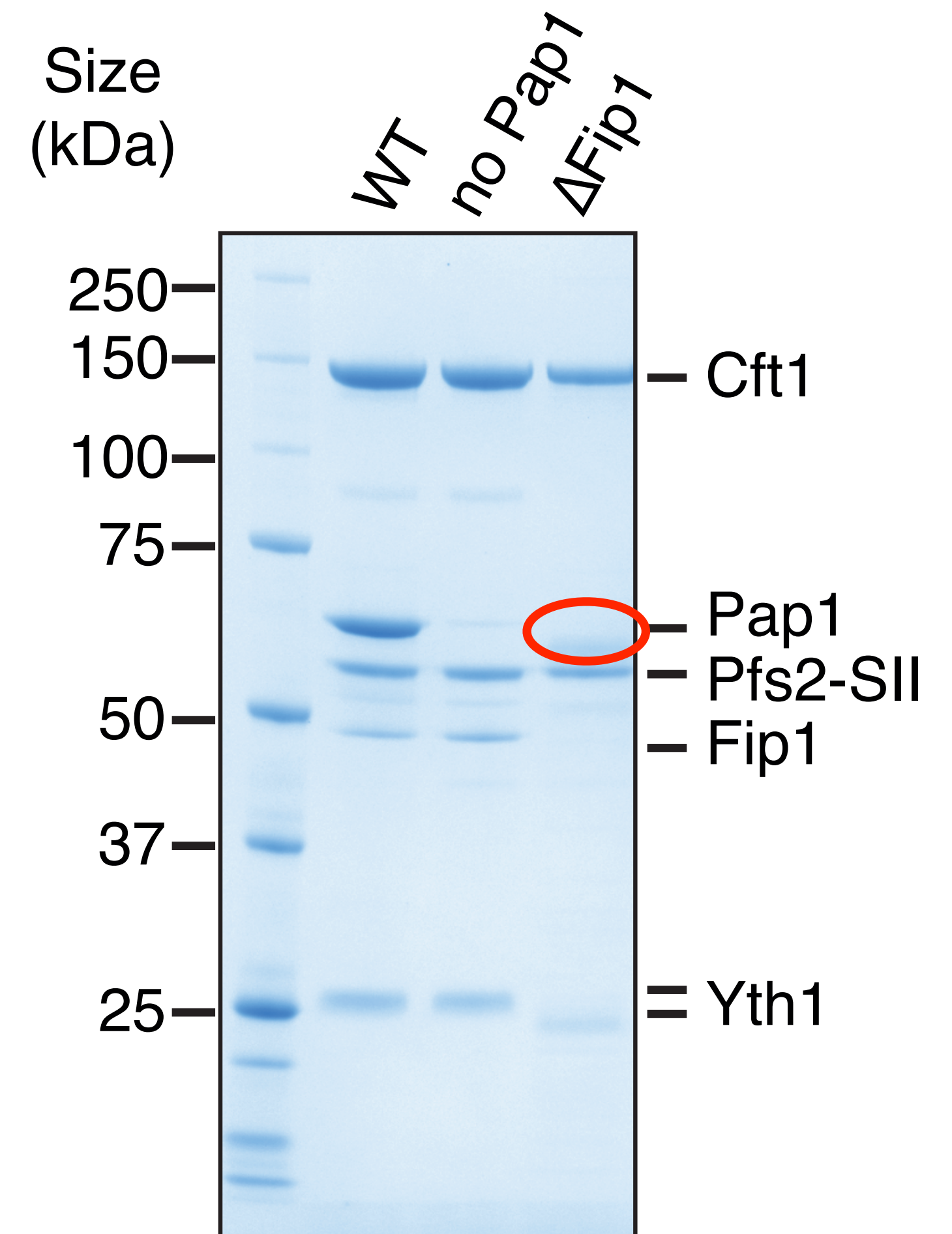
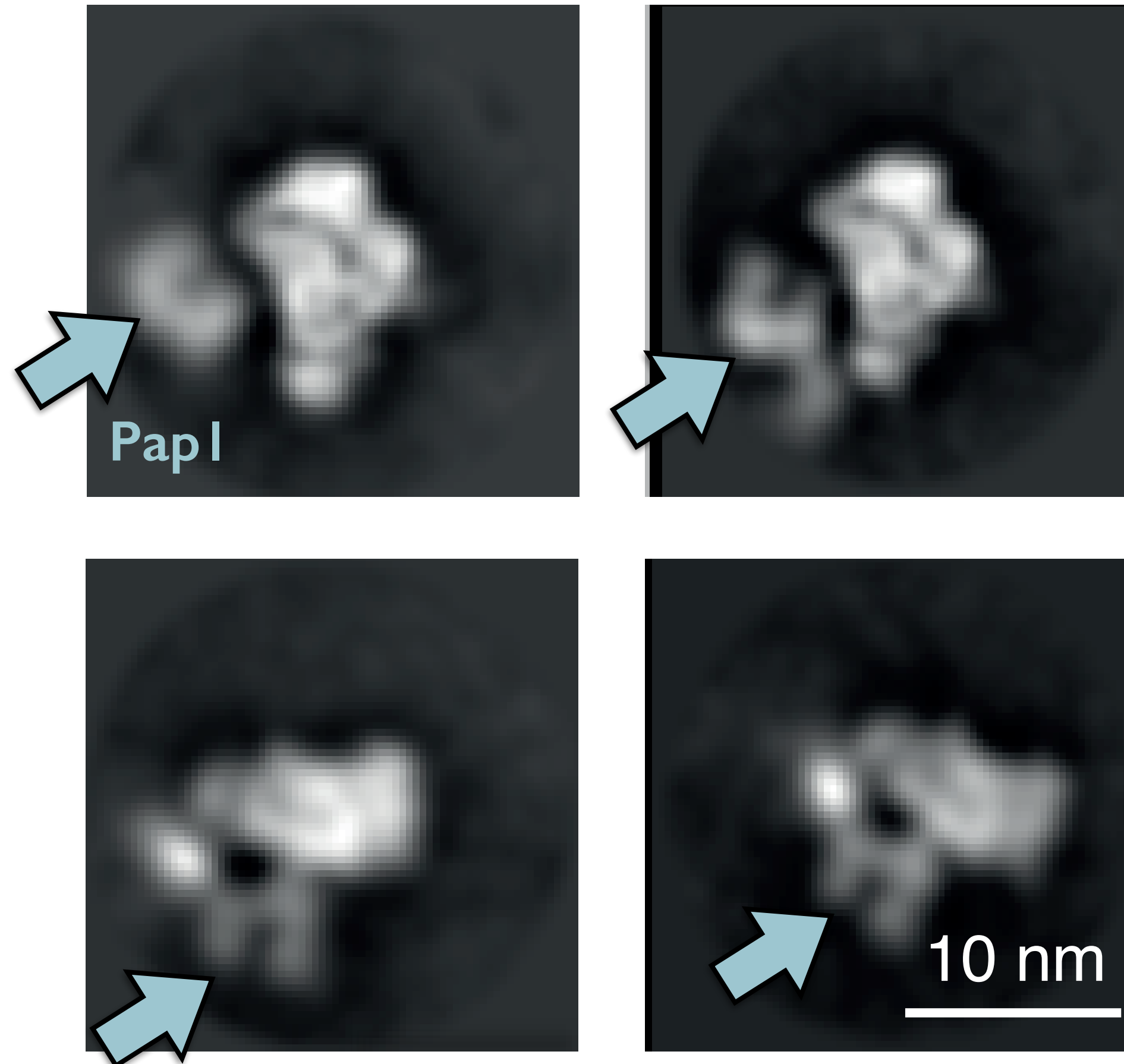
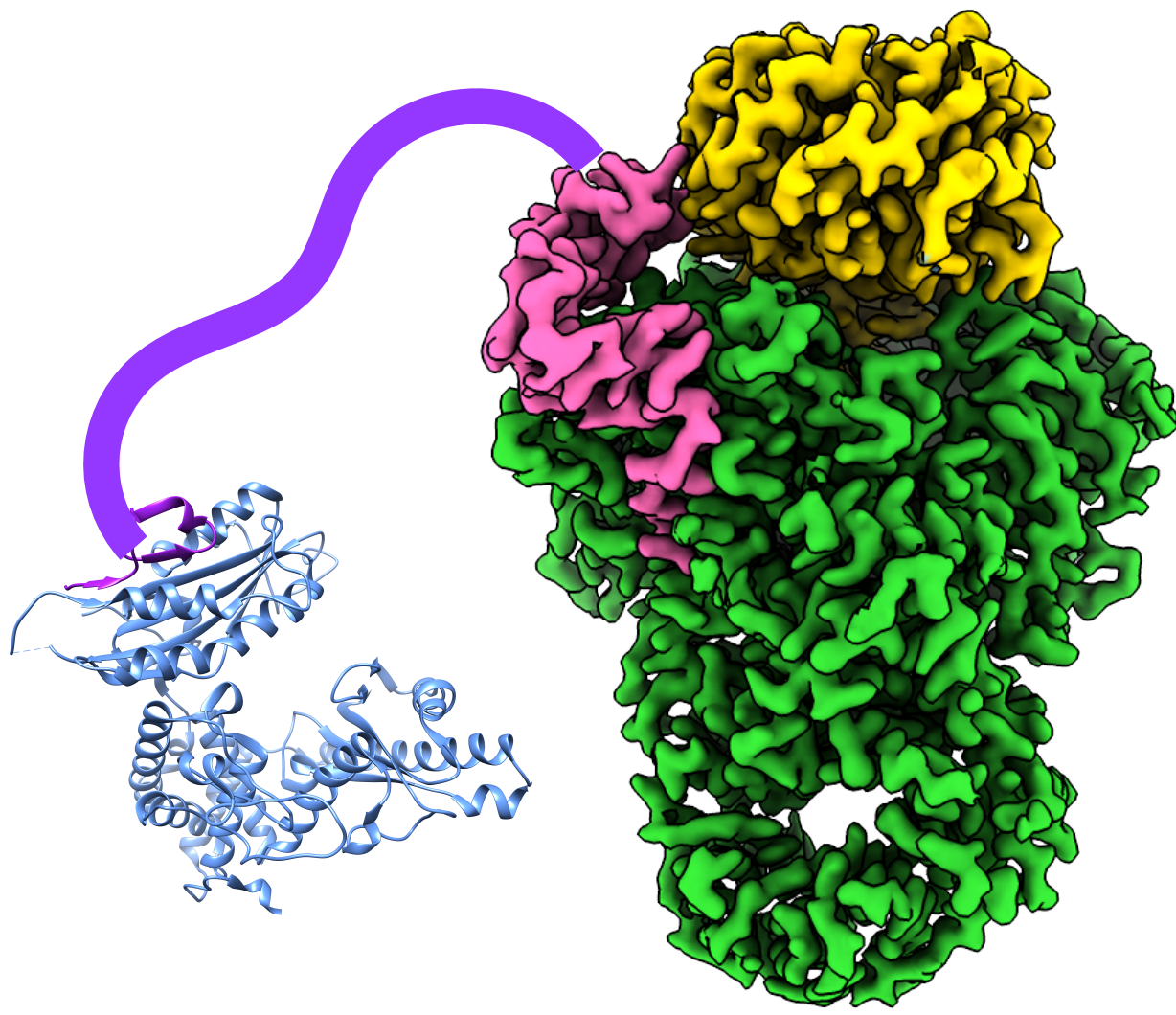
pre-mRNA splicing
SF3b

Scrima et al (2008)

Yan et al (2016)
Cretu et al (2016)
Plaschka et al (2017)

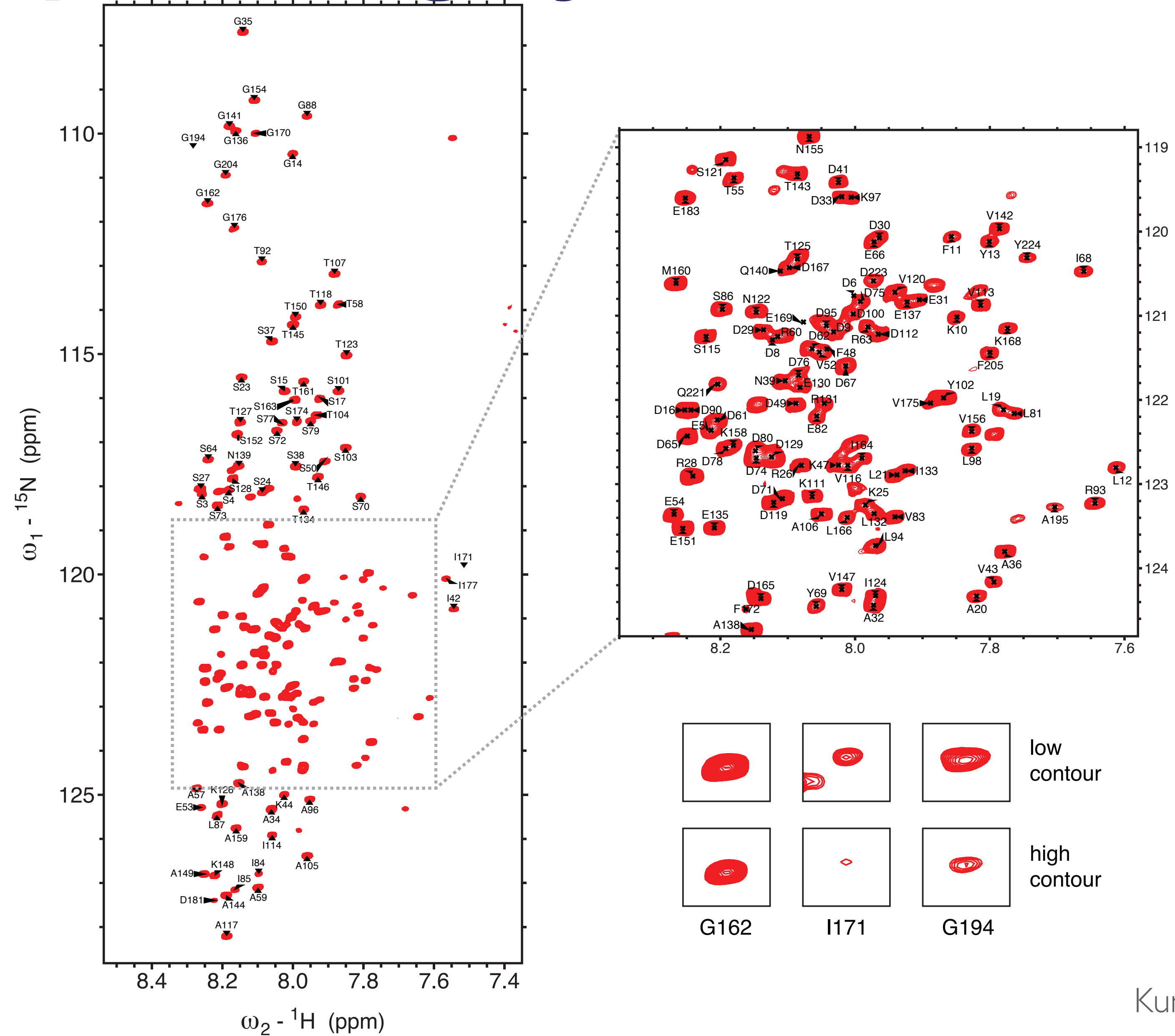
Pap1 is flexibly tethered

Pap1 is flexibly tethered



Ananth Kumar

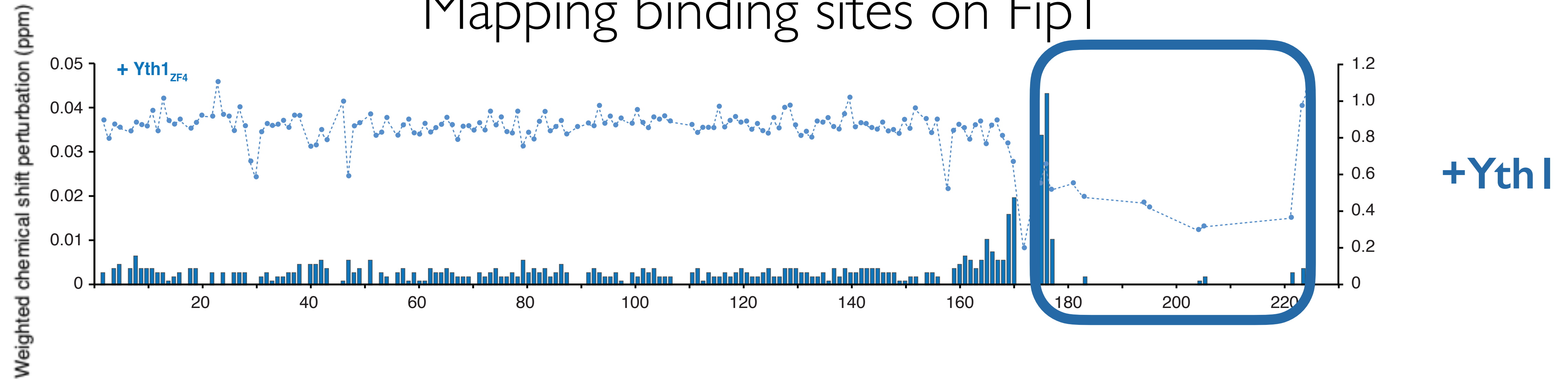
Fip1 is largely disordered



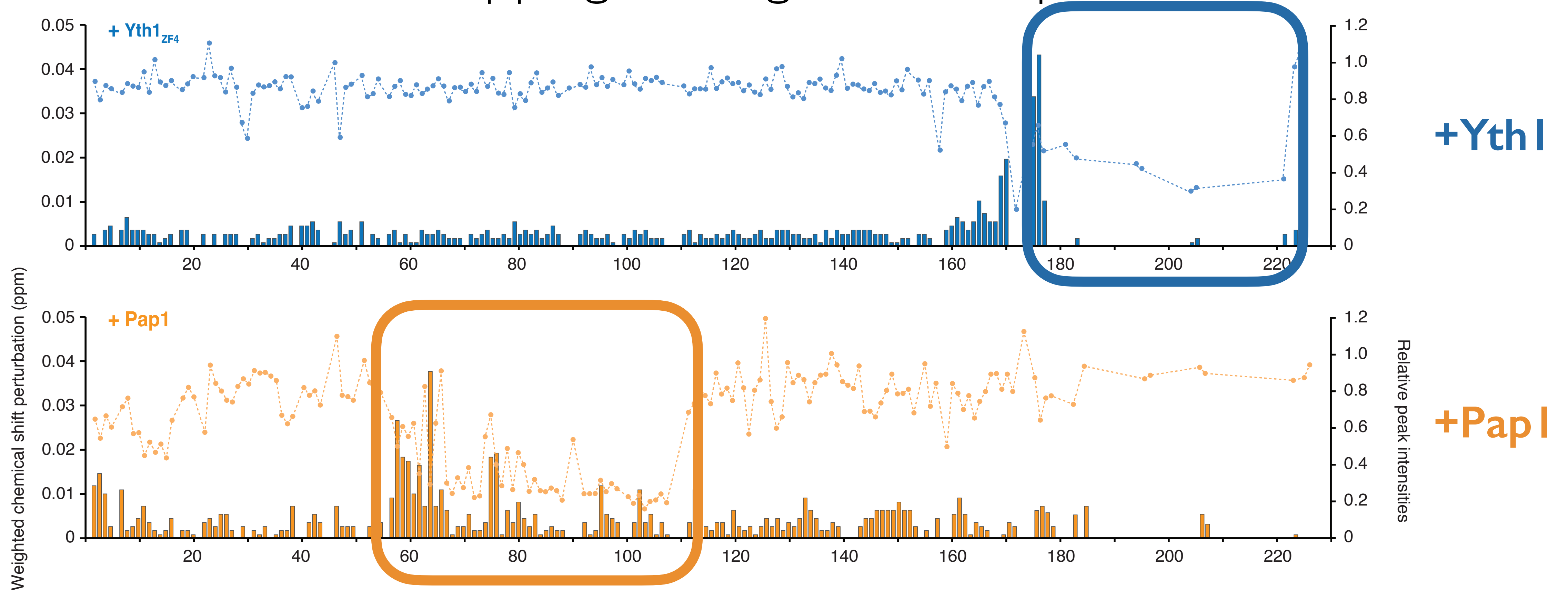
Ananth Kumar,
Conny Yu, Stefan Freund



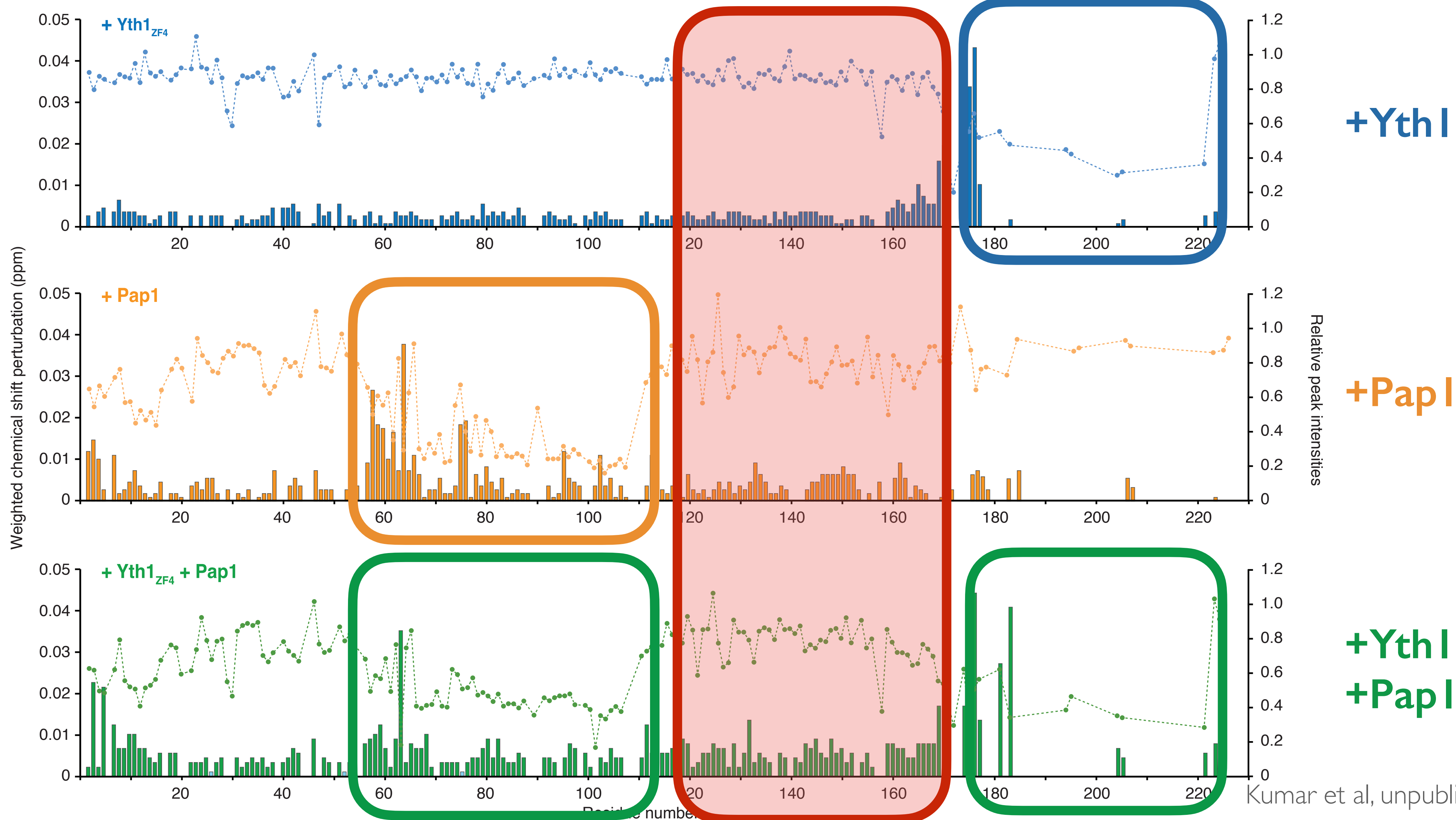
Mapping binding sites on Fip I



Mapping binding sites on Fip I



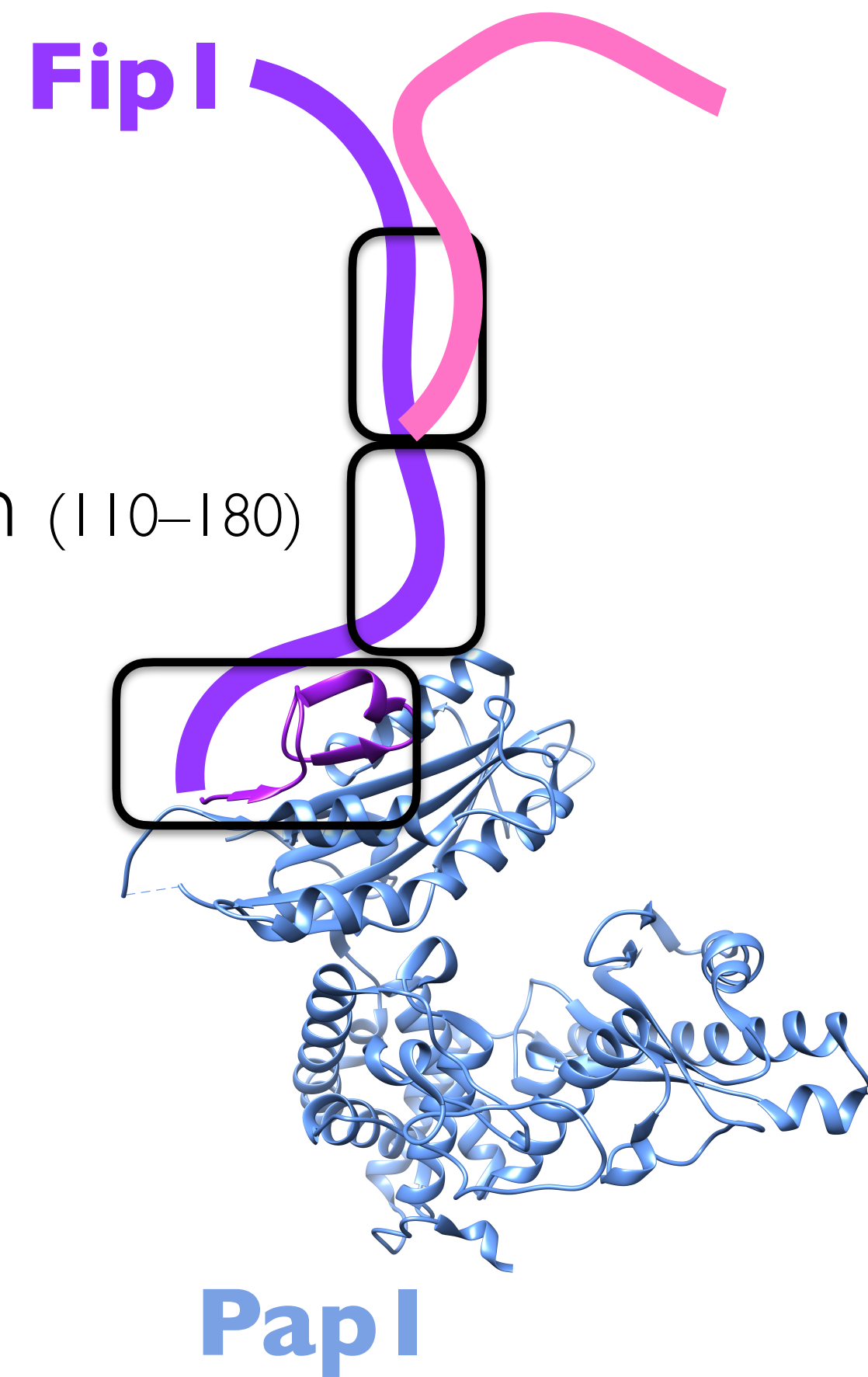
Mapping binding sites on Fip I



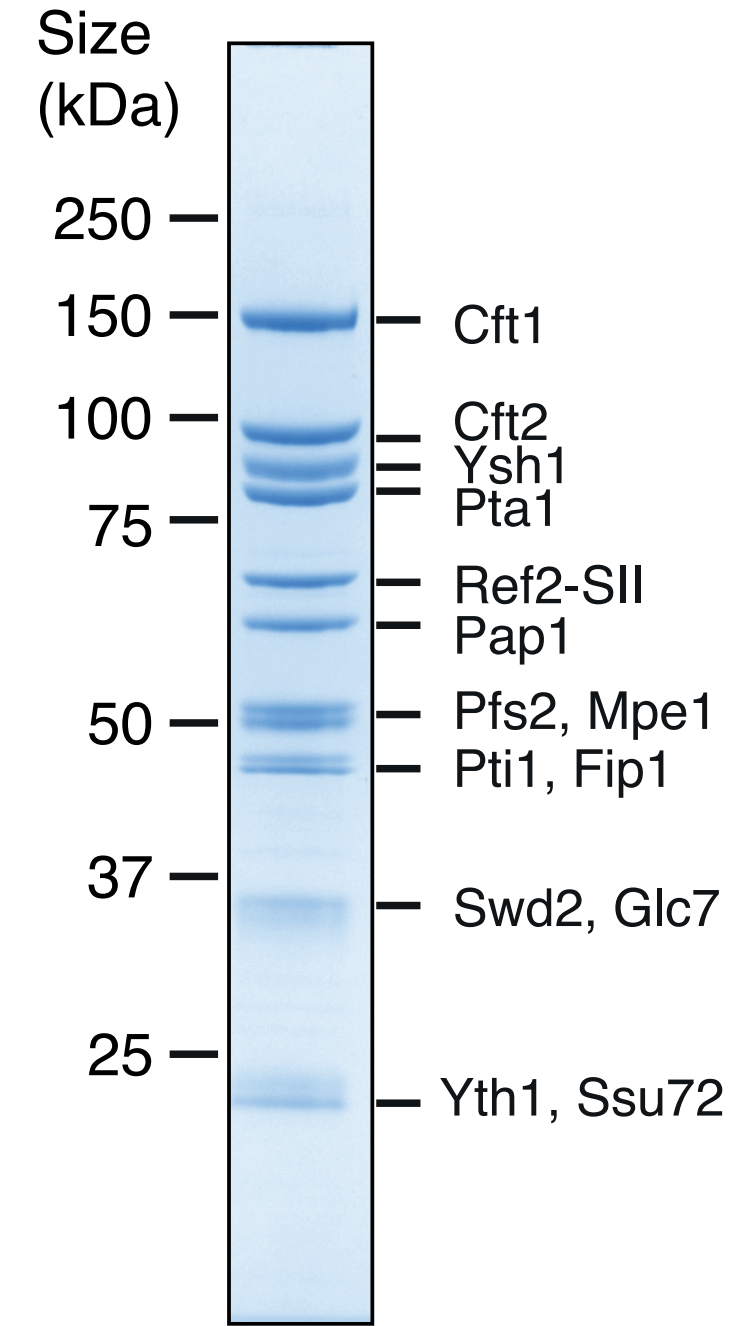
Yth I binding (180–220)
Hamilton & Tong 2020

Low complexity region (110–180)
Ezeokonkwo et al., 2011

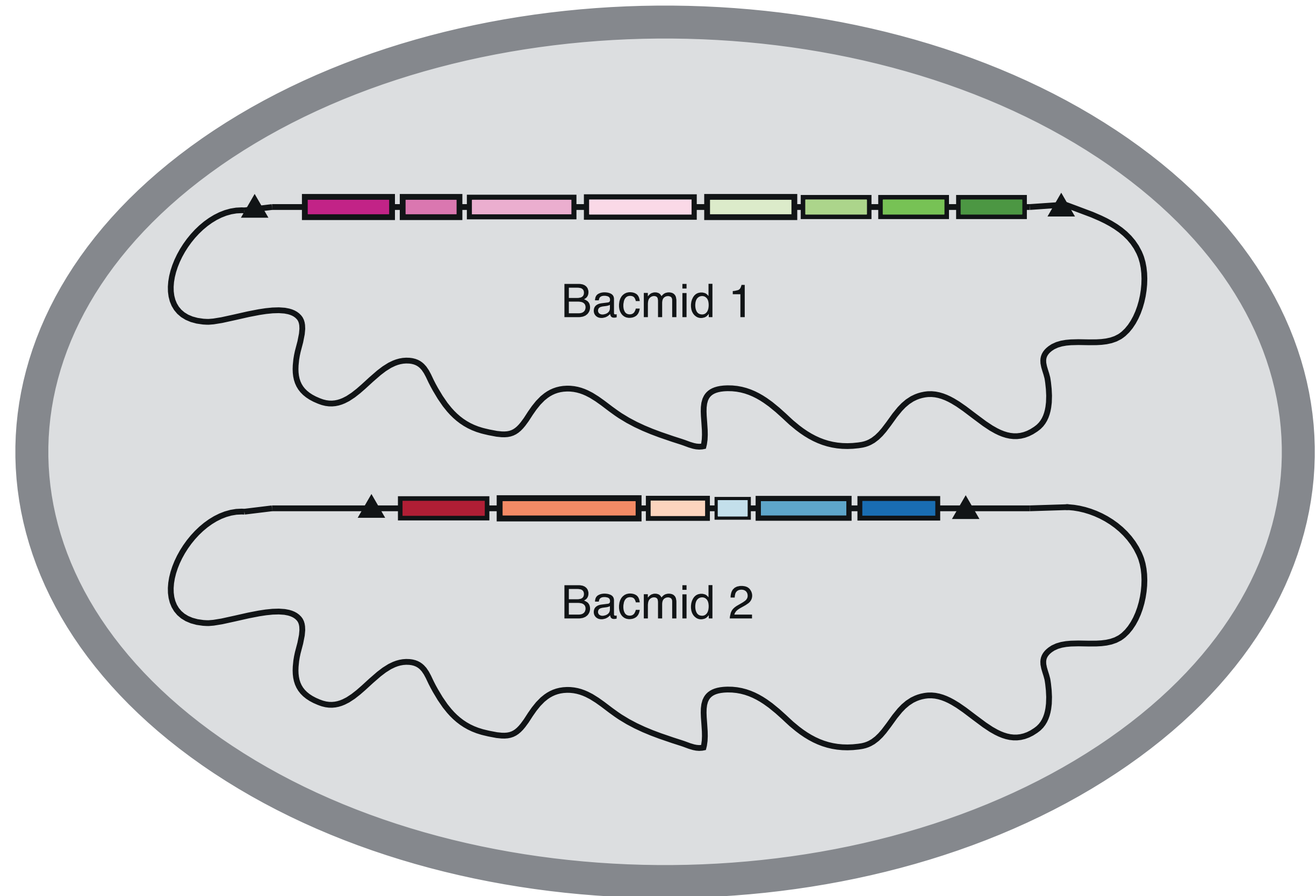
Pap I binding (60–110)
Meinke et al., 2008



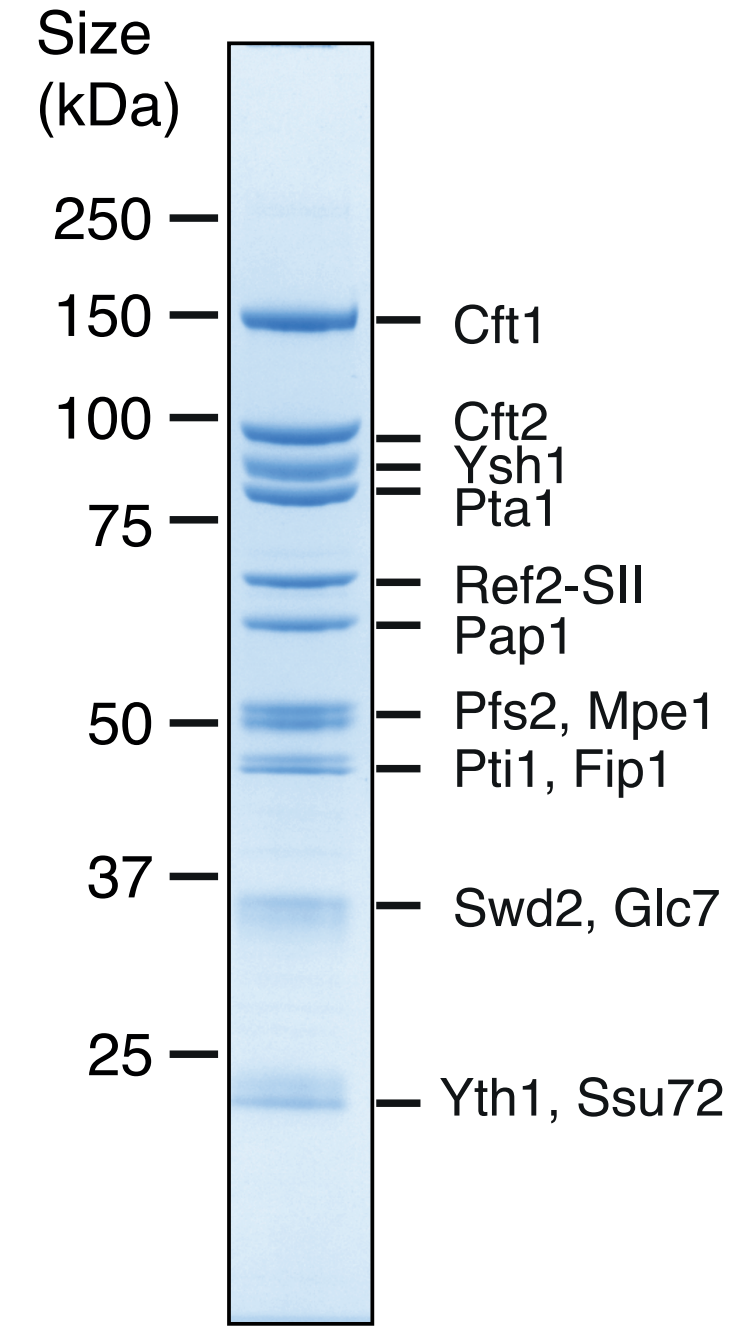
Understanding the dynamics of CPF



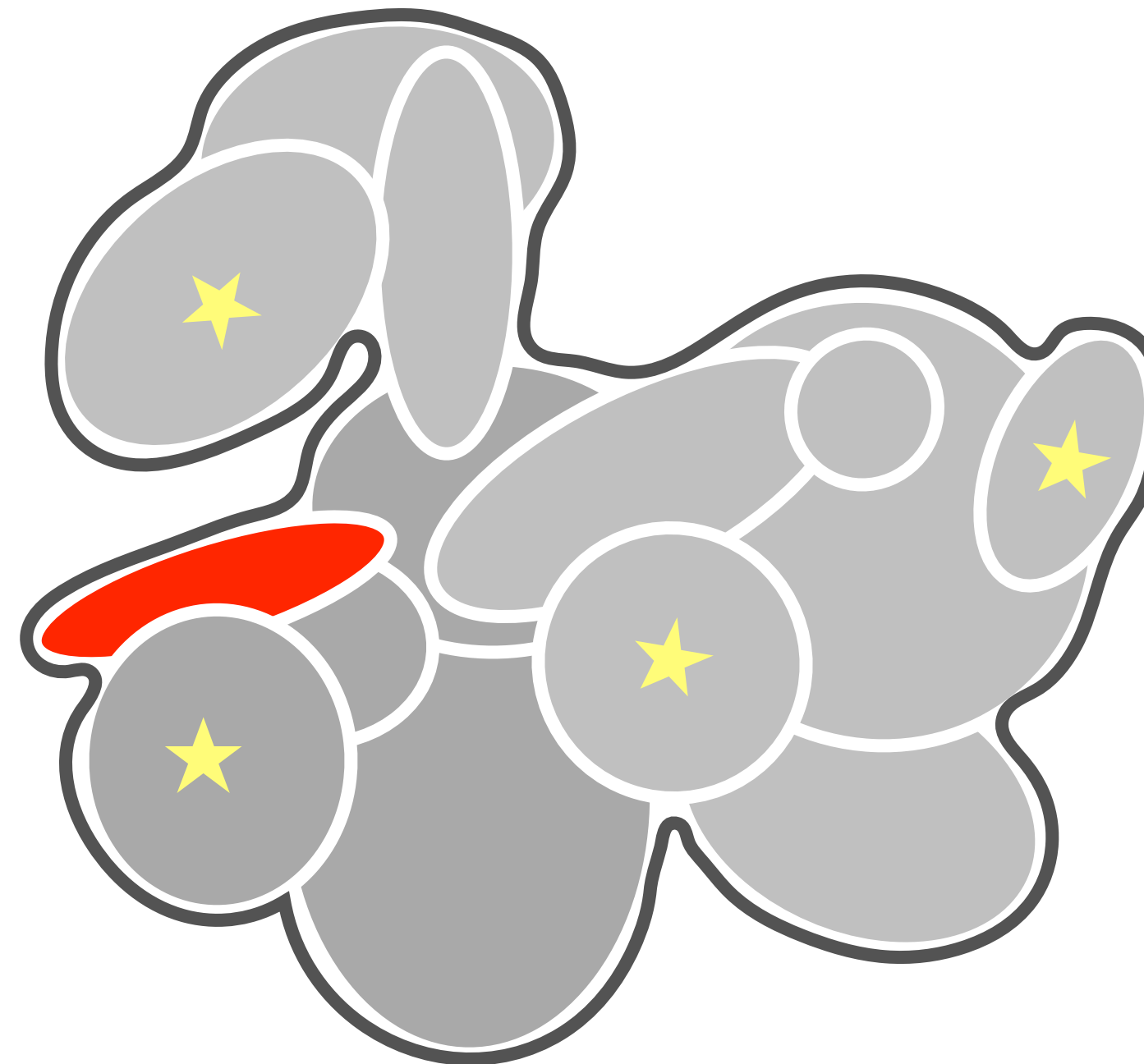
Recombinant
CPF



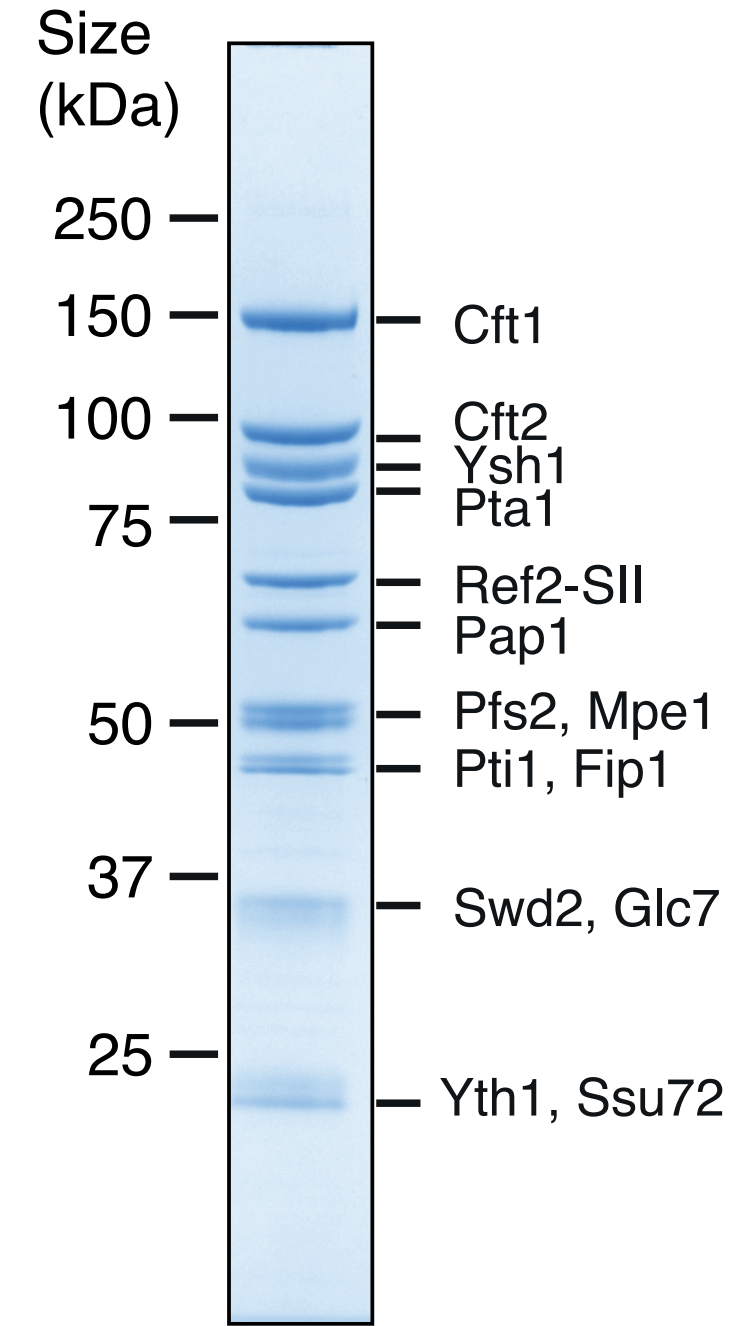
Understanding the dynamics of CPF



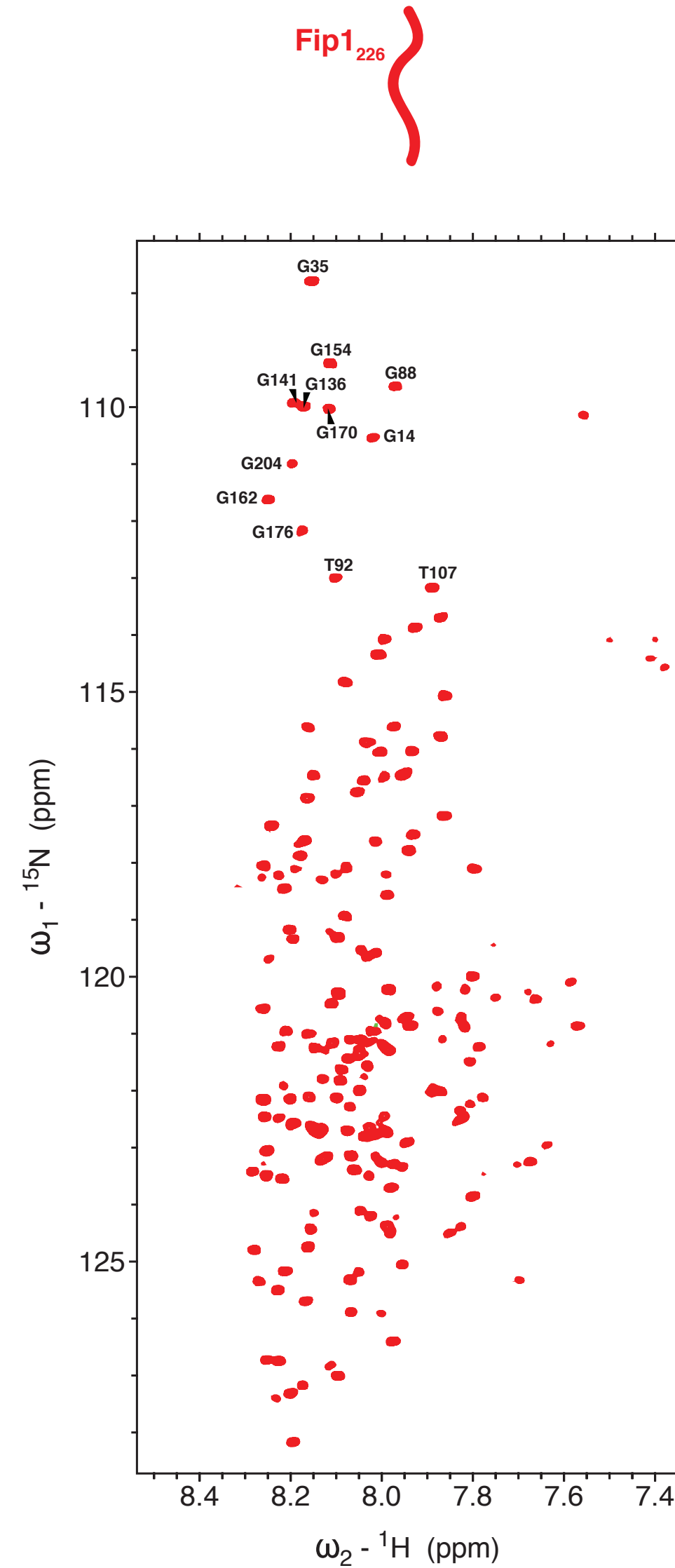
Recombinant
CPF



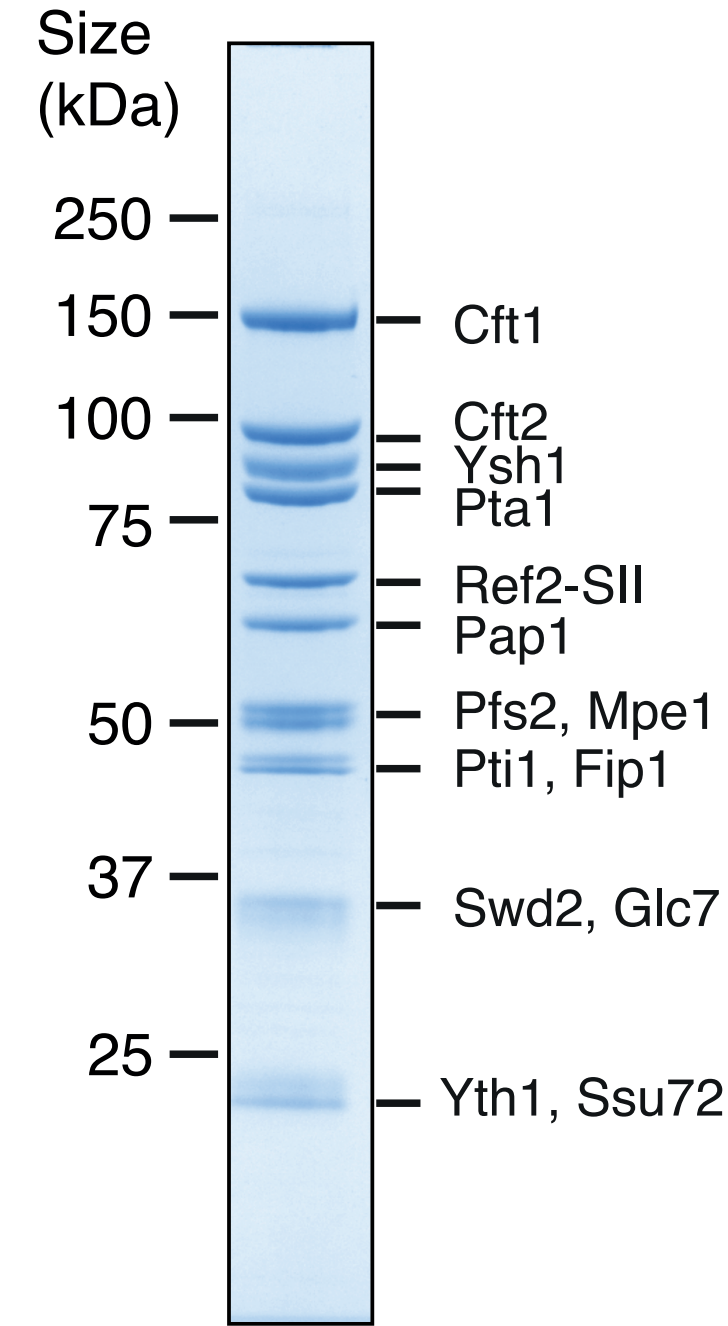
Understanding the dynamics of CPF



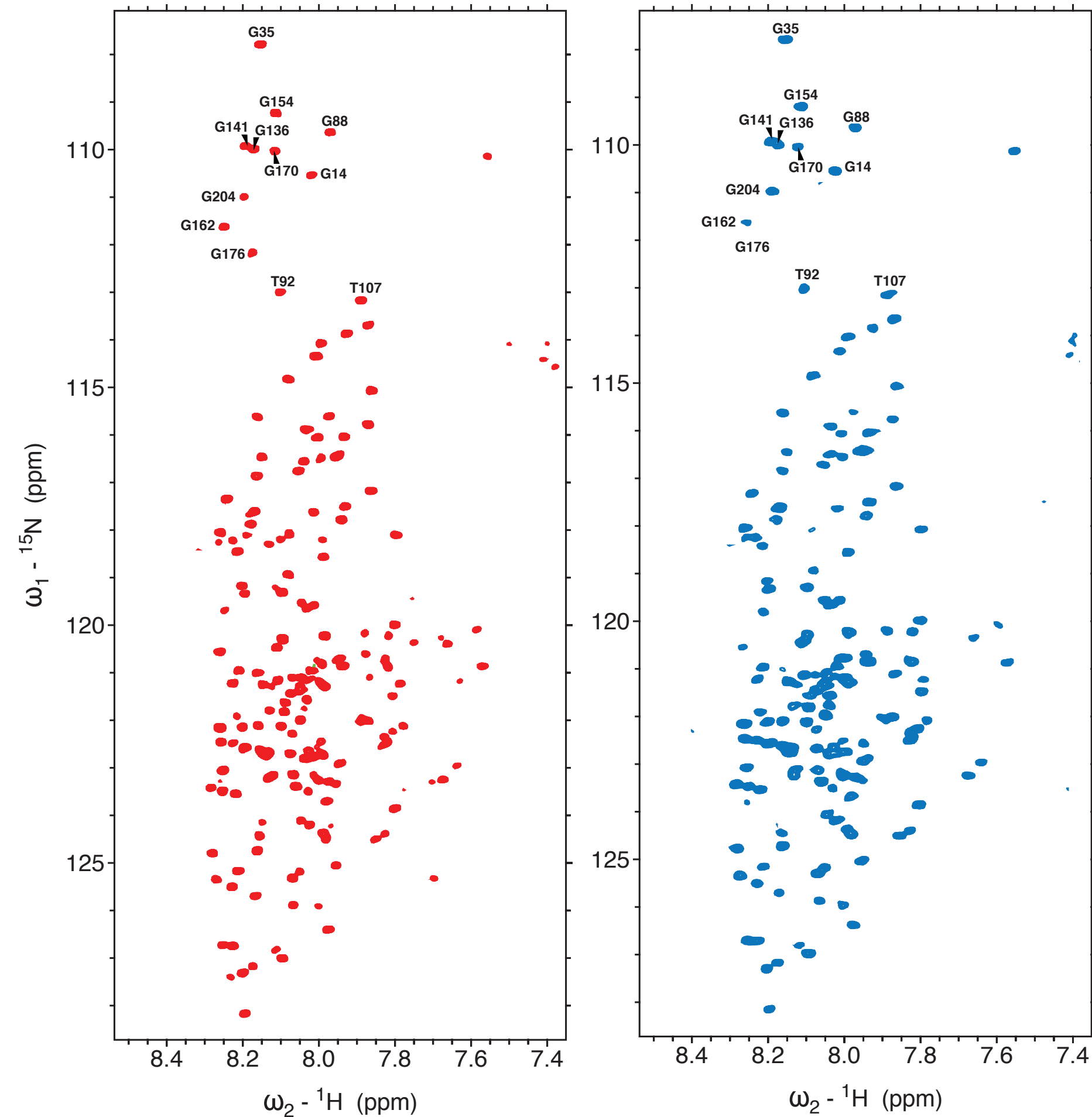
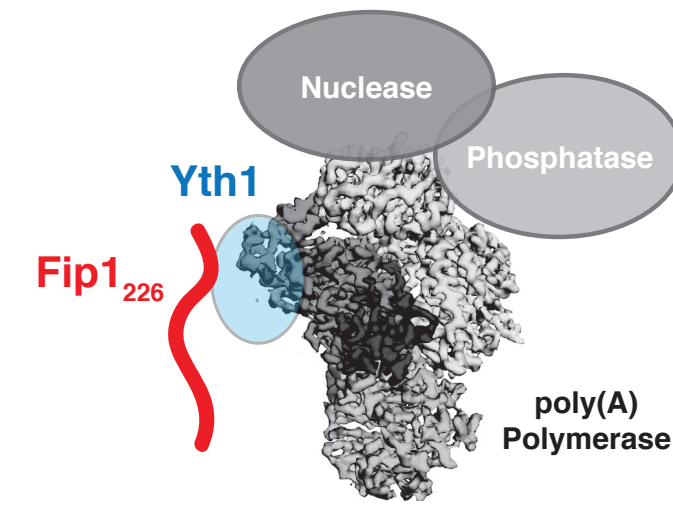
Recombinant
CPF



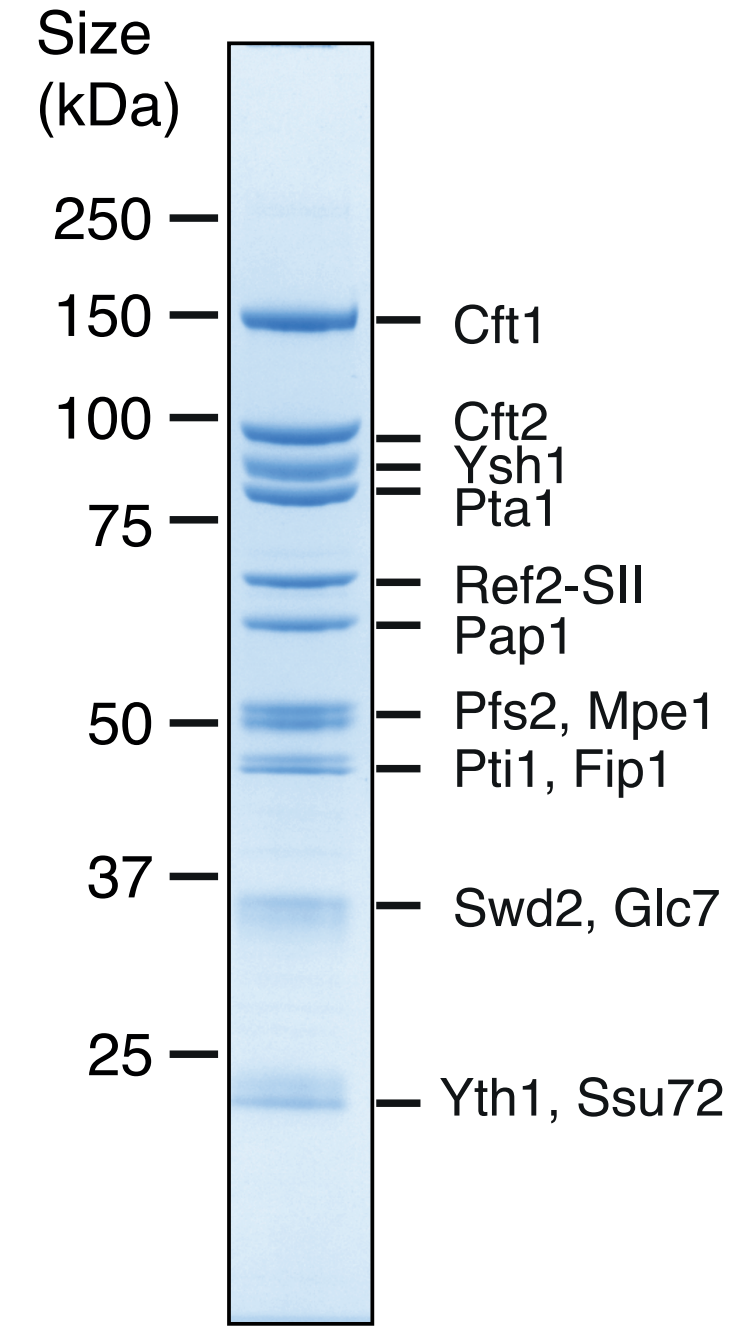
Understanding the dynamics of CPF



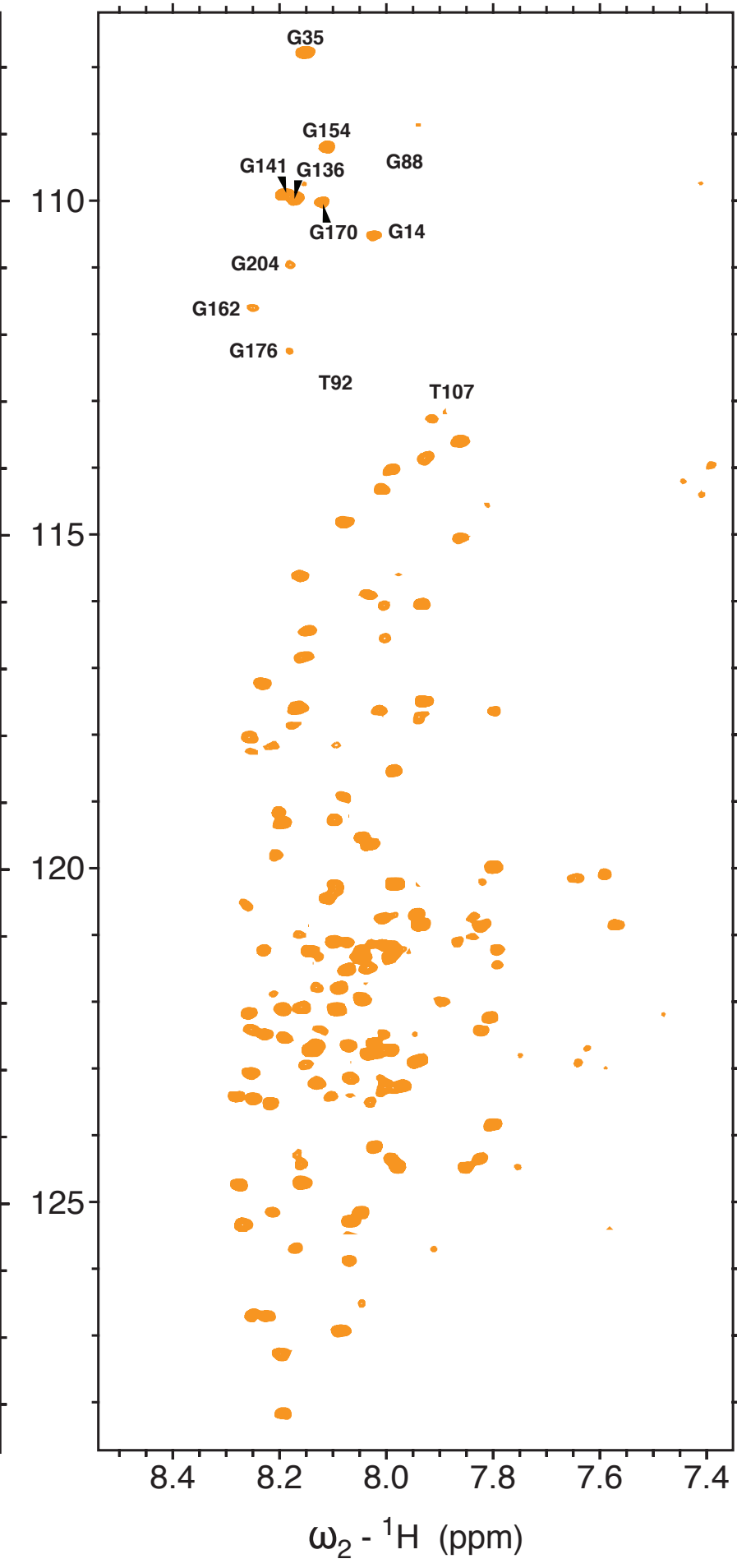
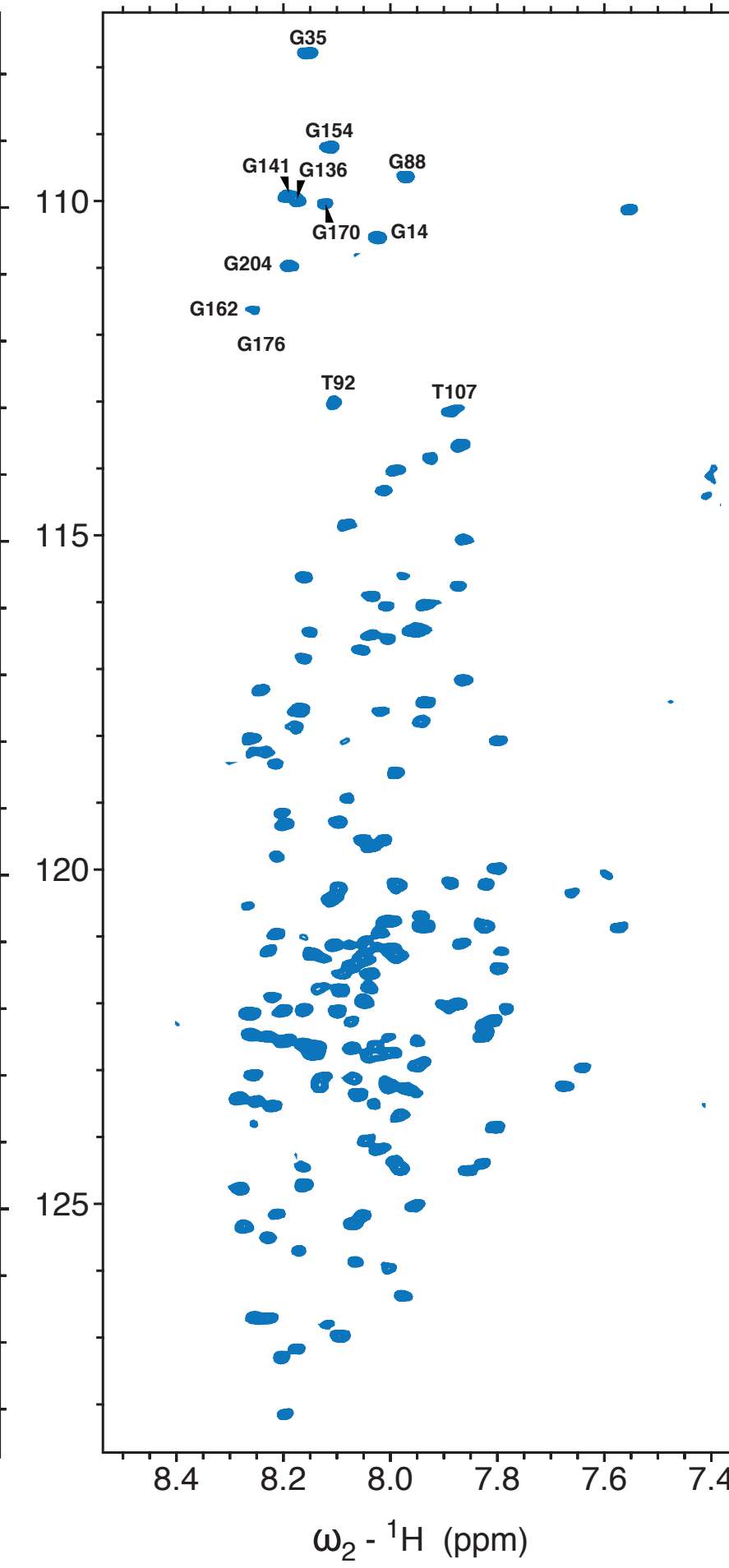
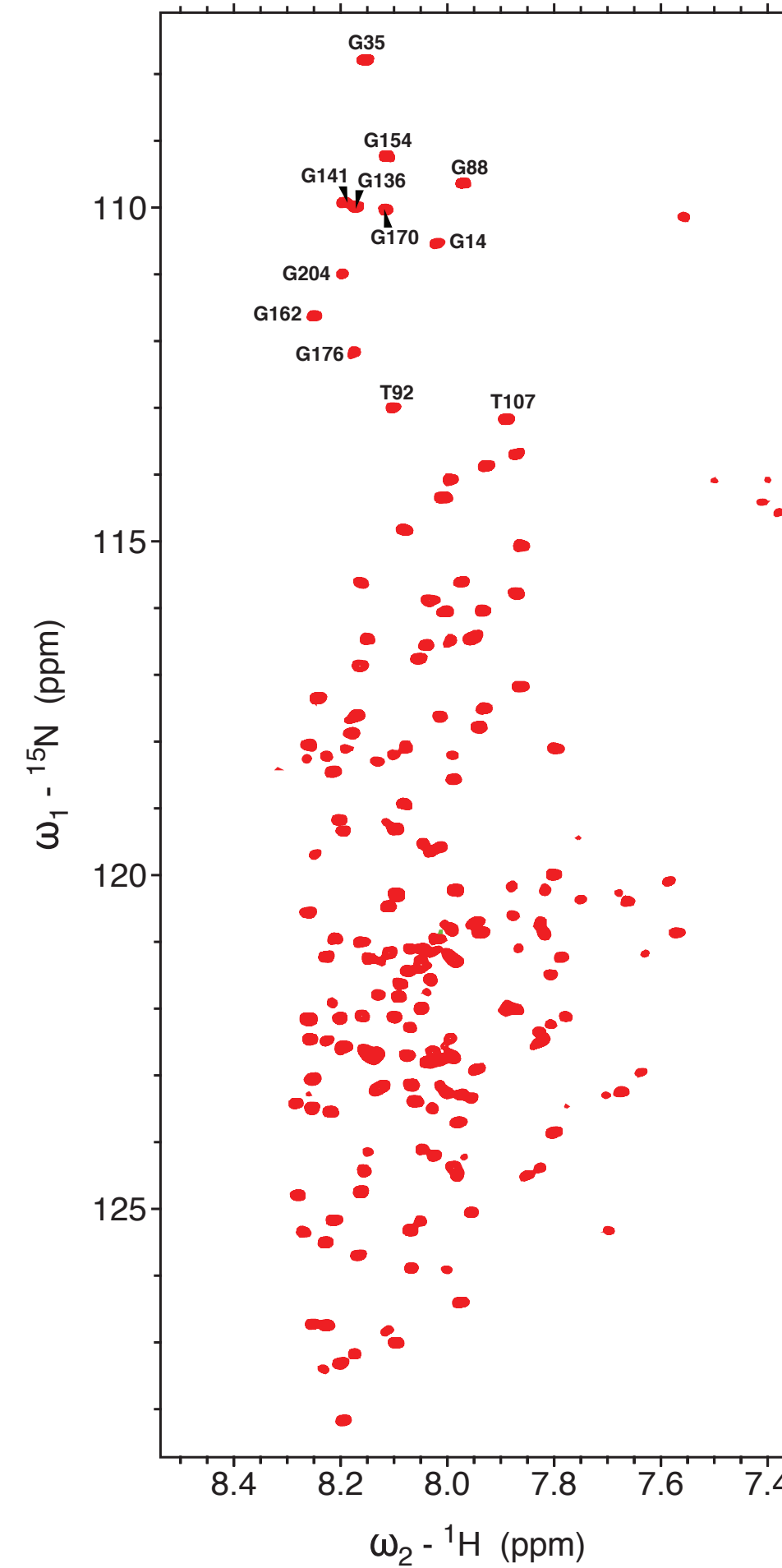
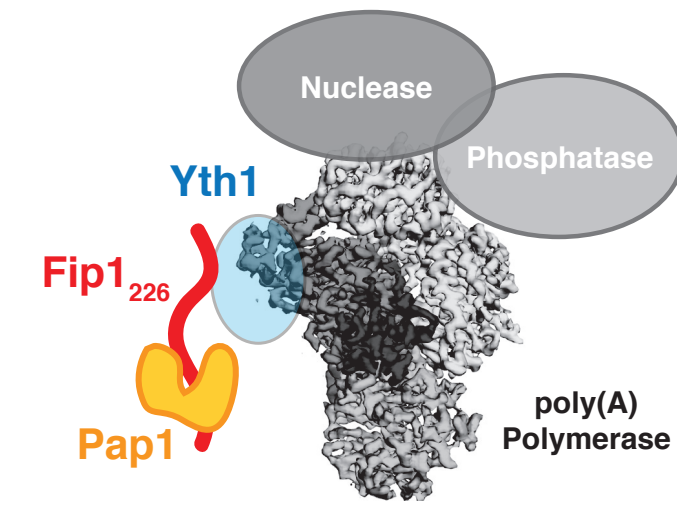
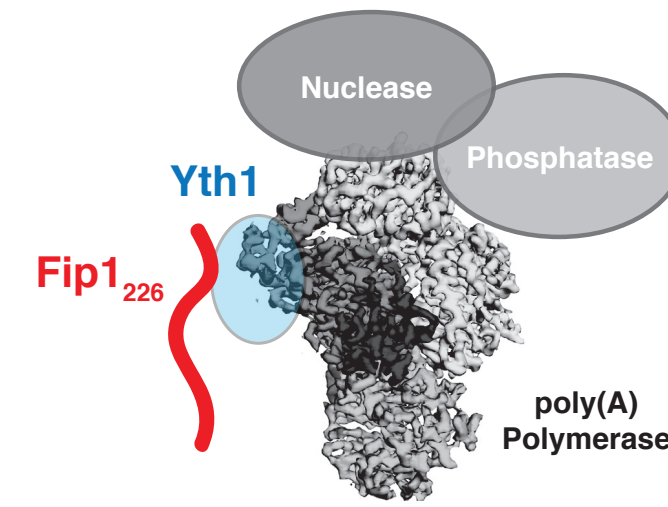
Recombinant
CPF



Understanding the dynamics of CPF



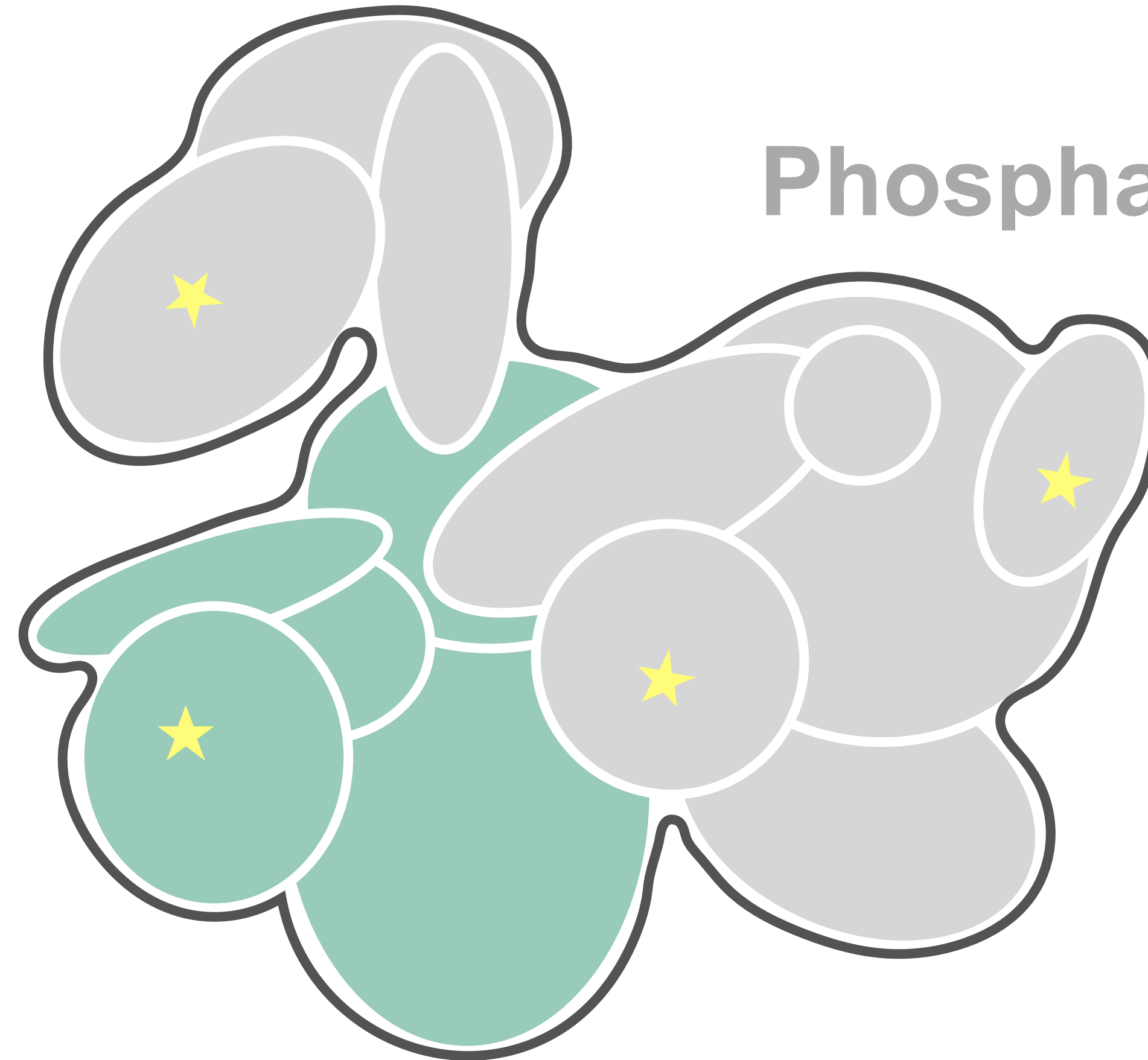
Recombinant
CPF



How is the nuclease activated?

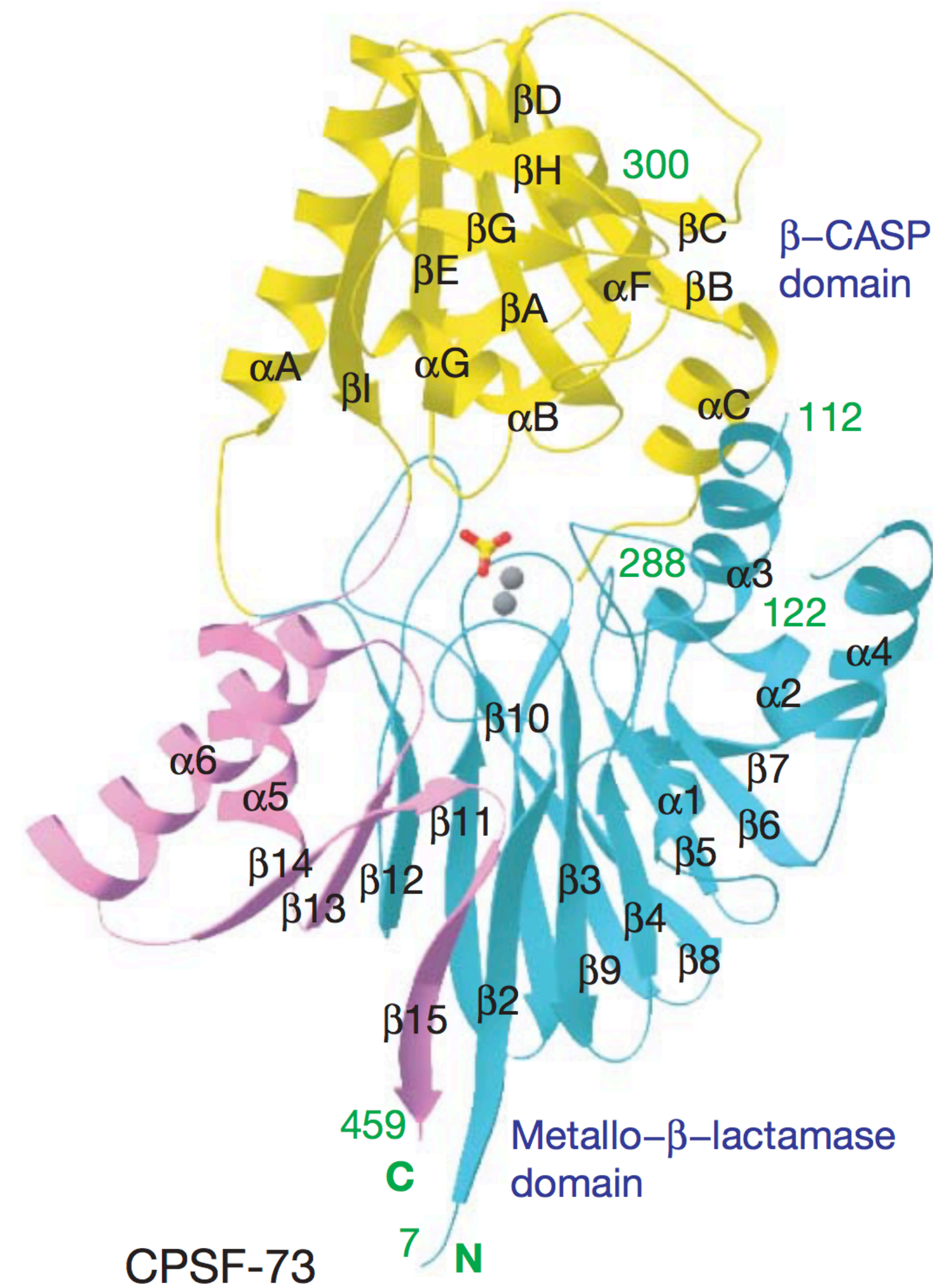
Nuclease

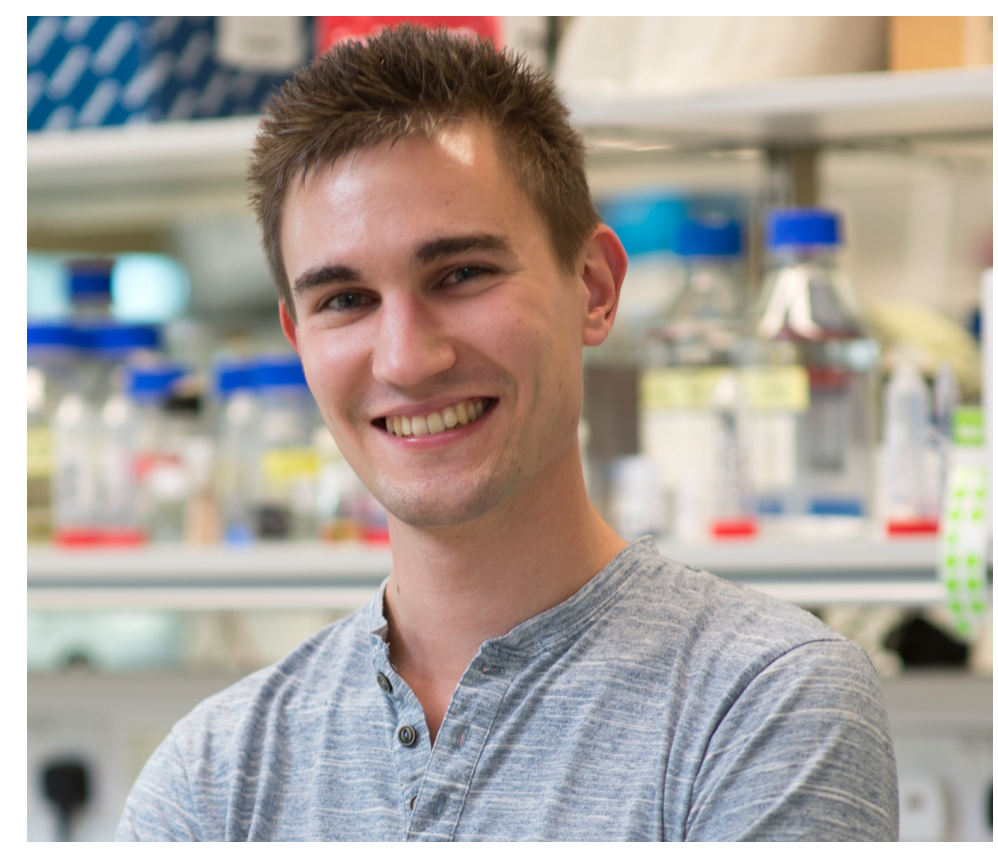
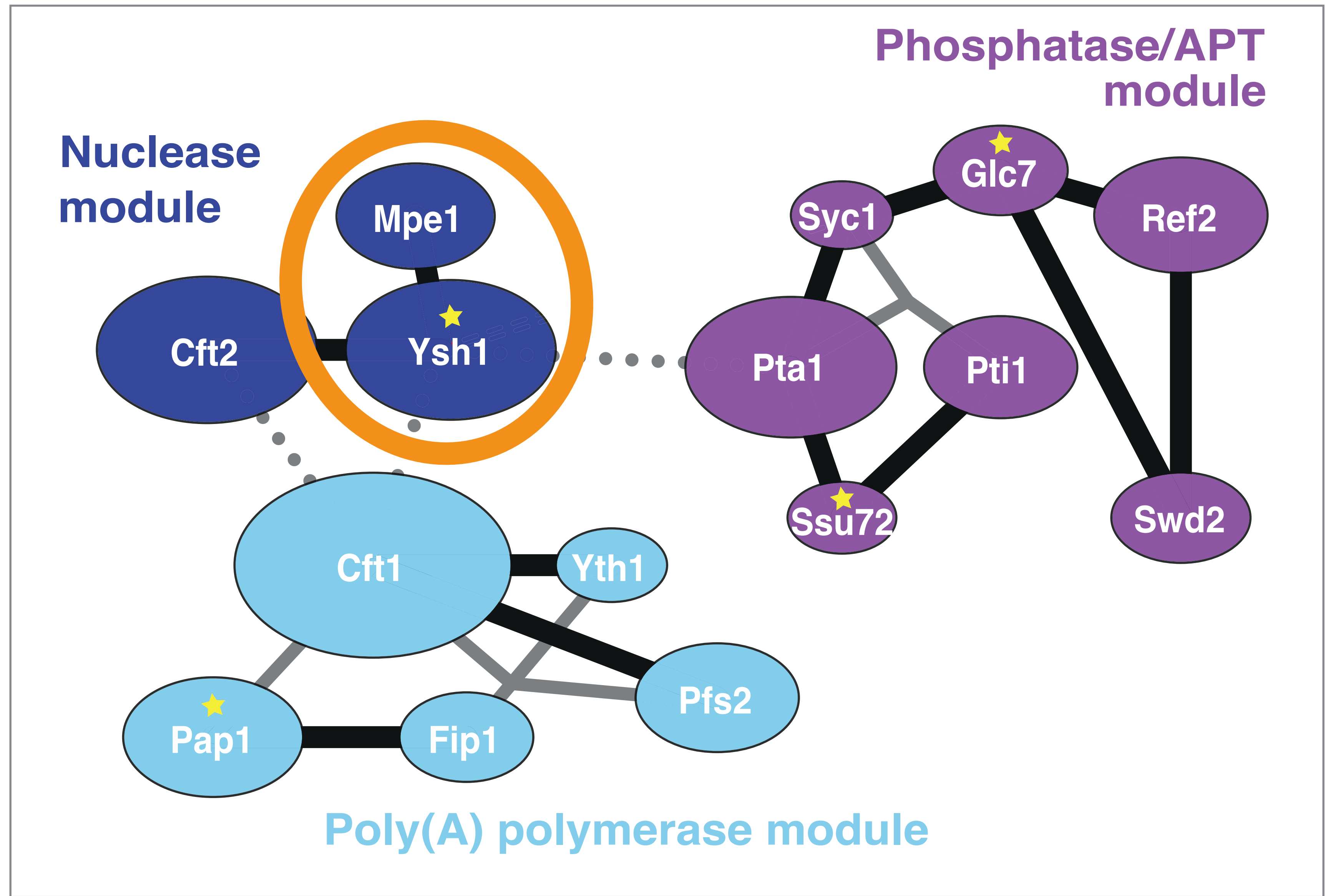
Phosphatase



Poly(A) polymerase

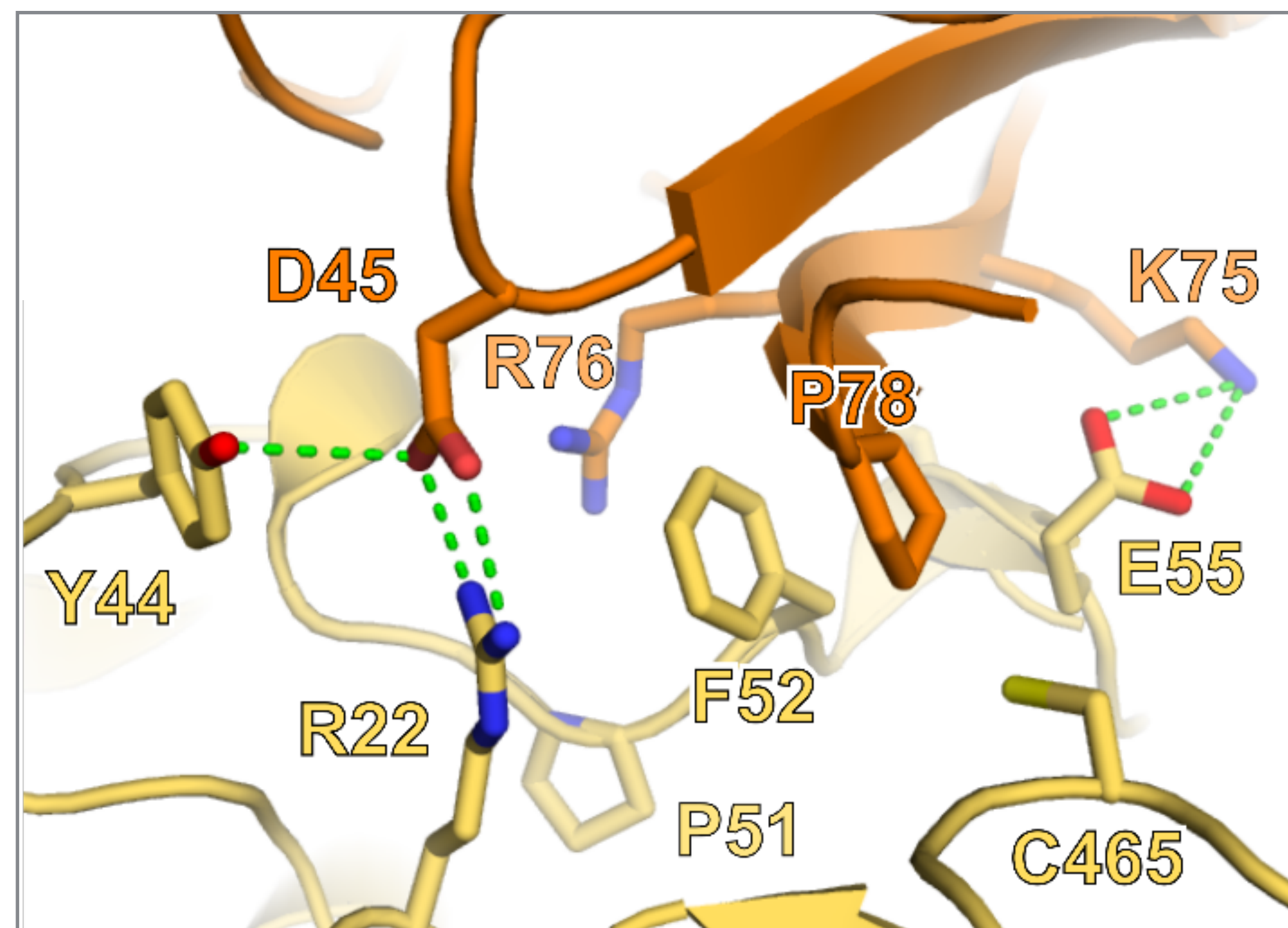
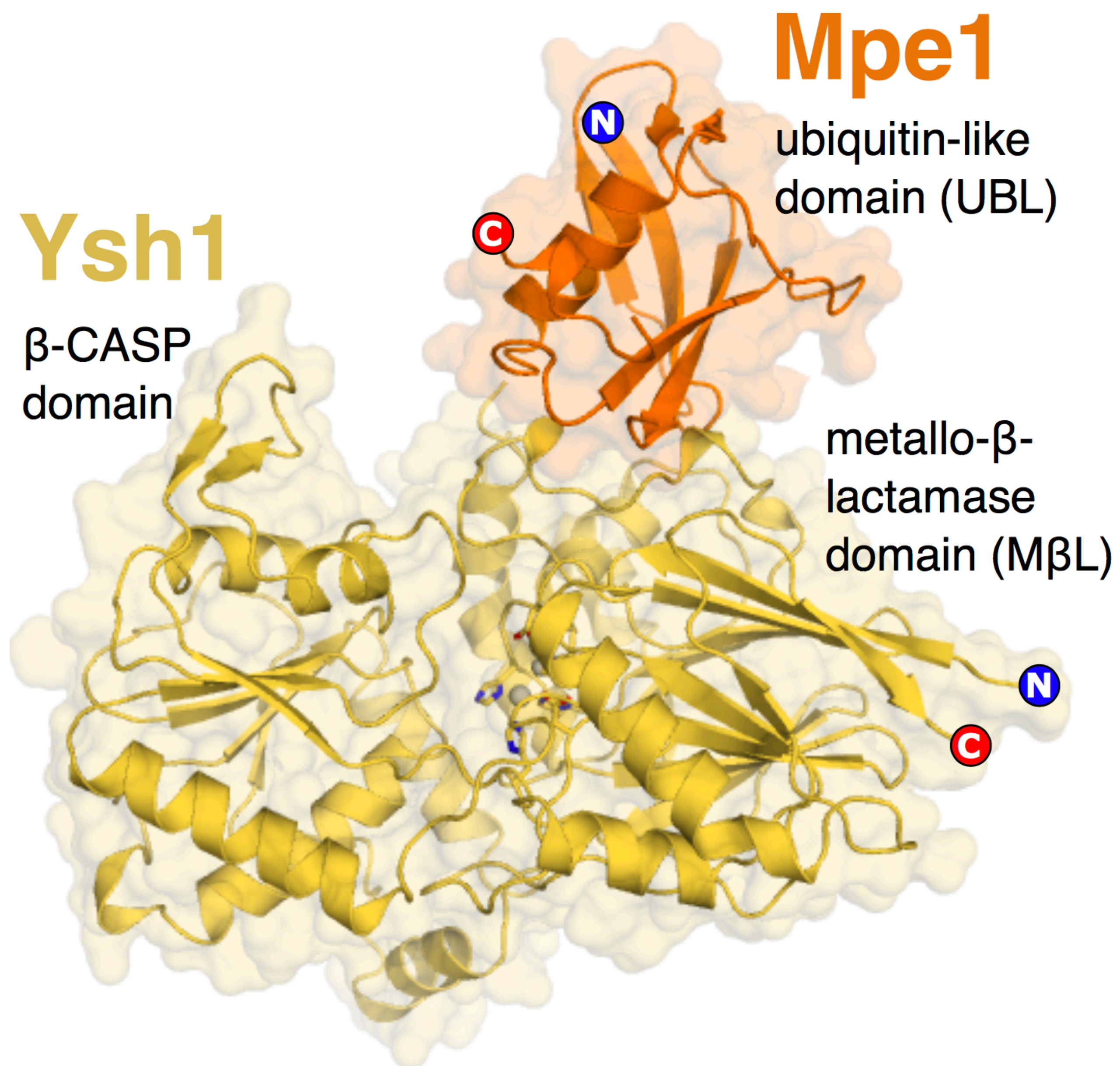
CPF nuclease



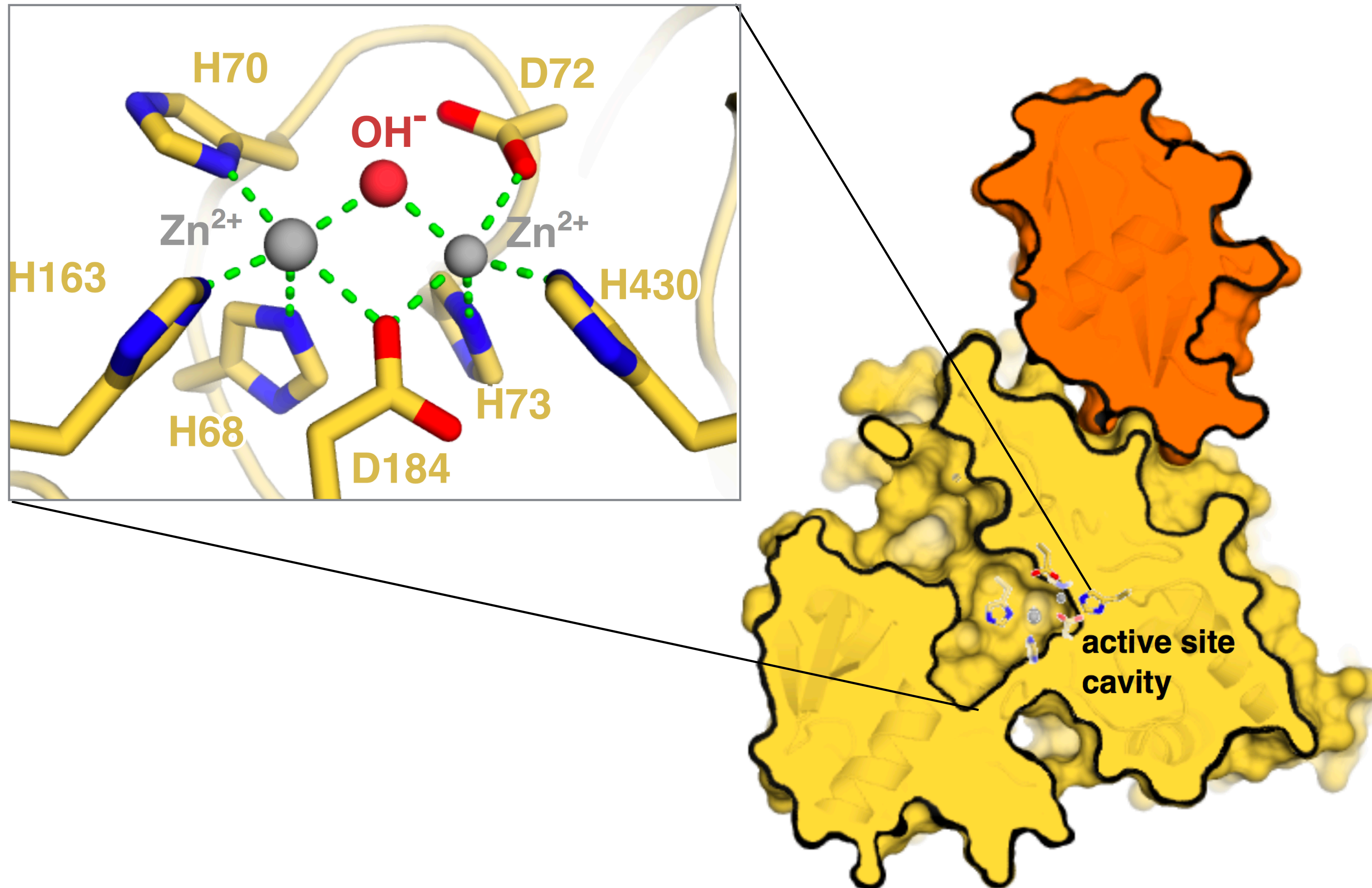


Chris Hill

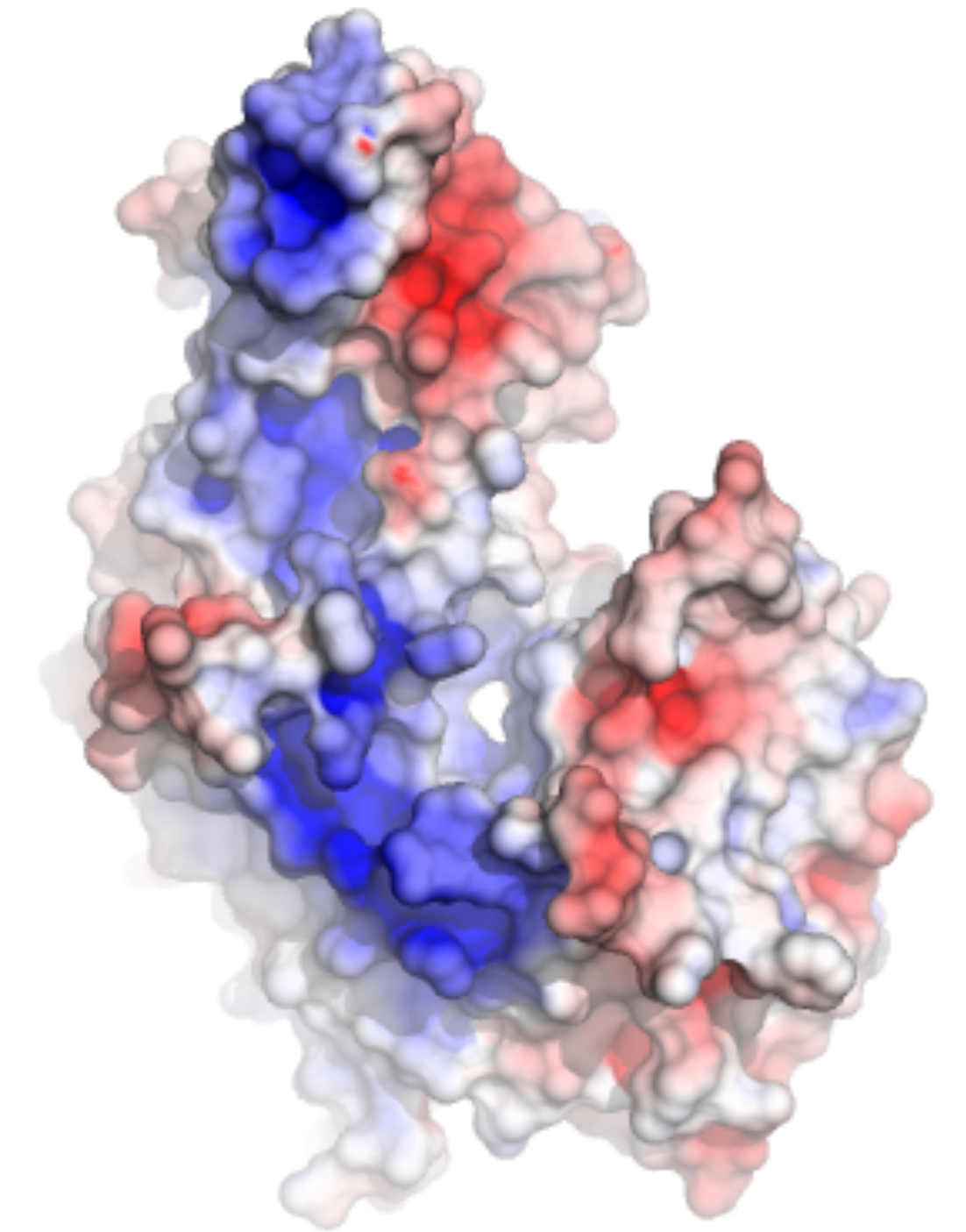
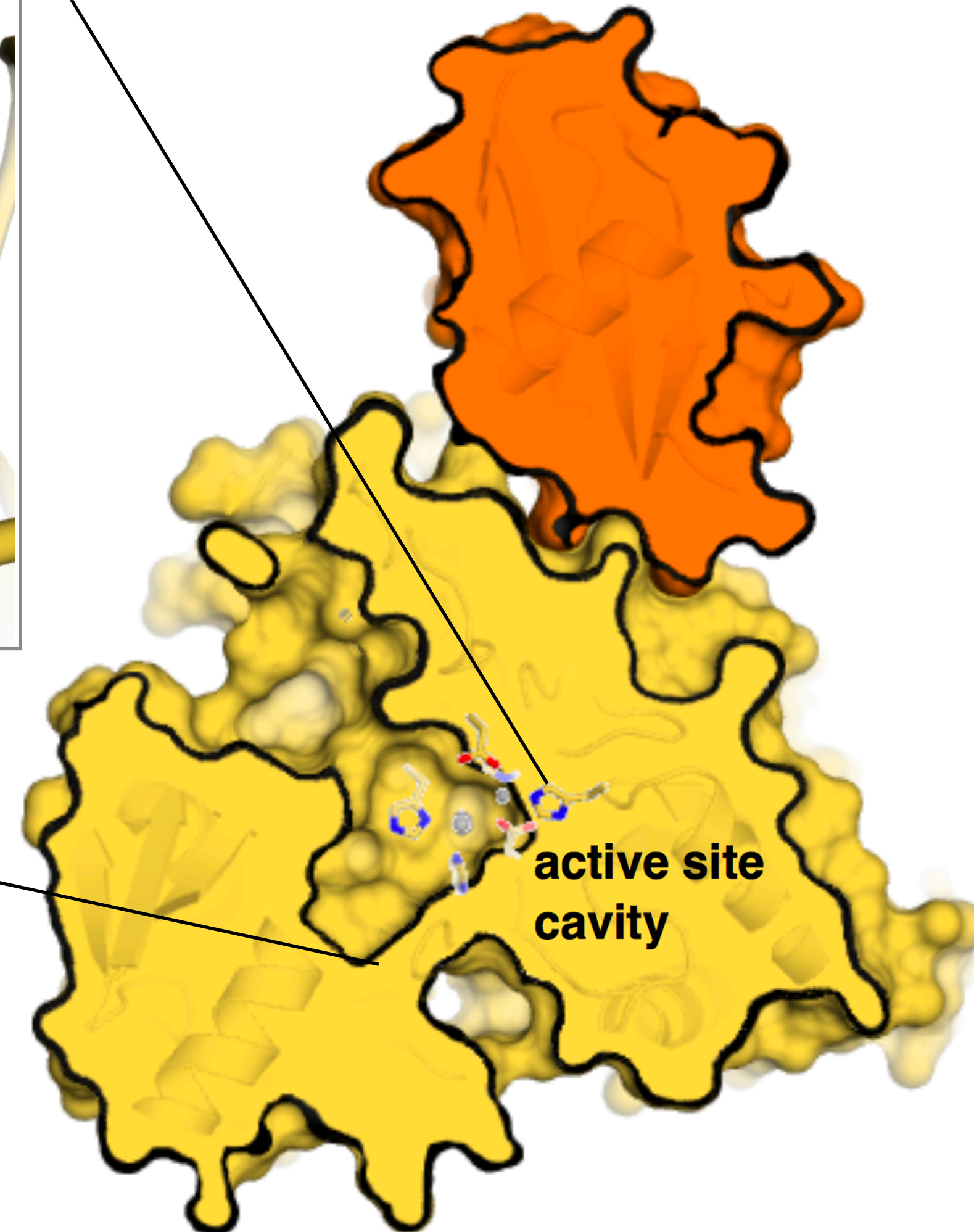
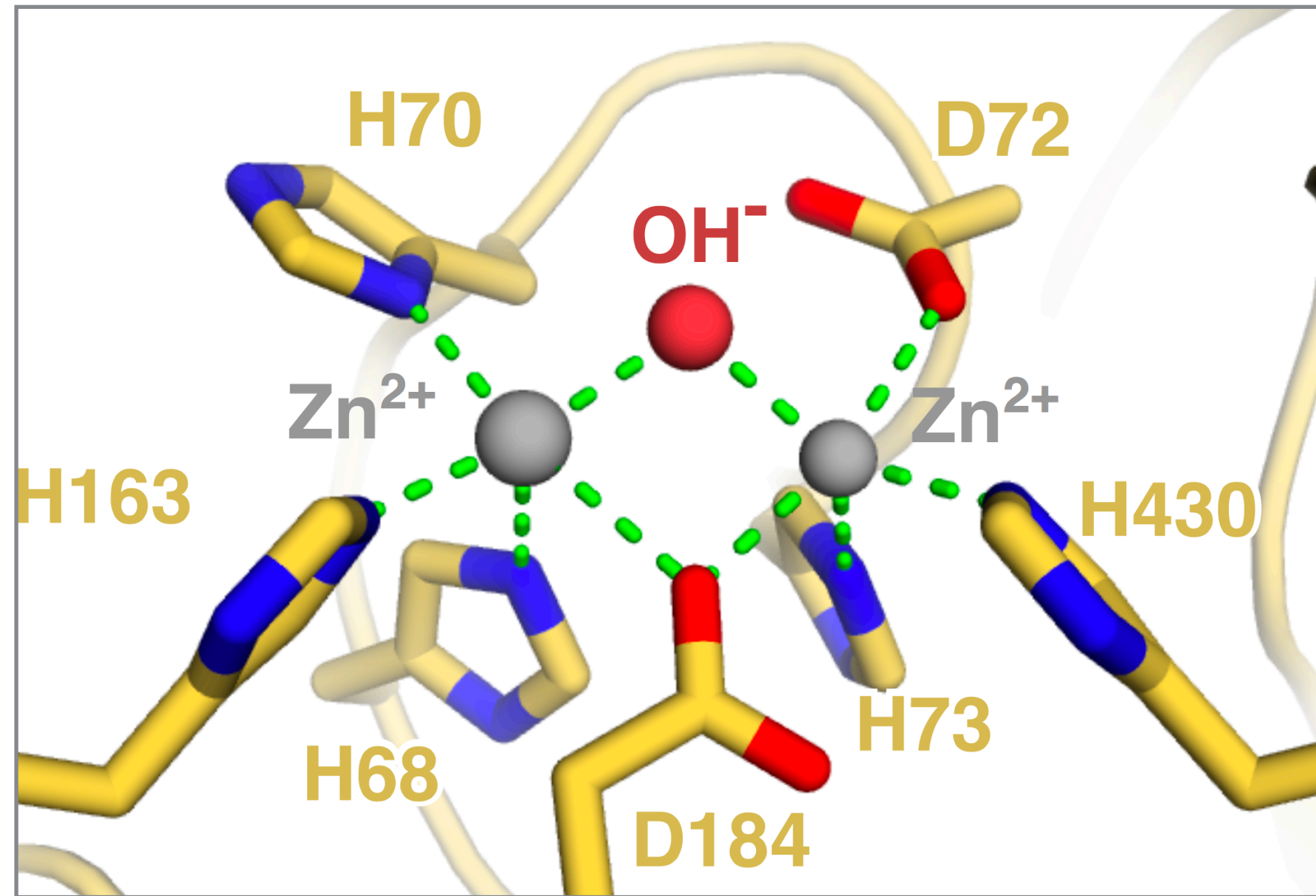
X-ray crystal and cryoEM structure of Ysh I-Mpe I complex



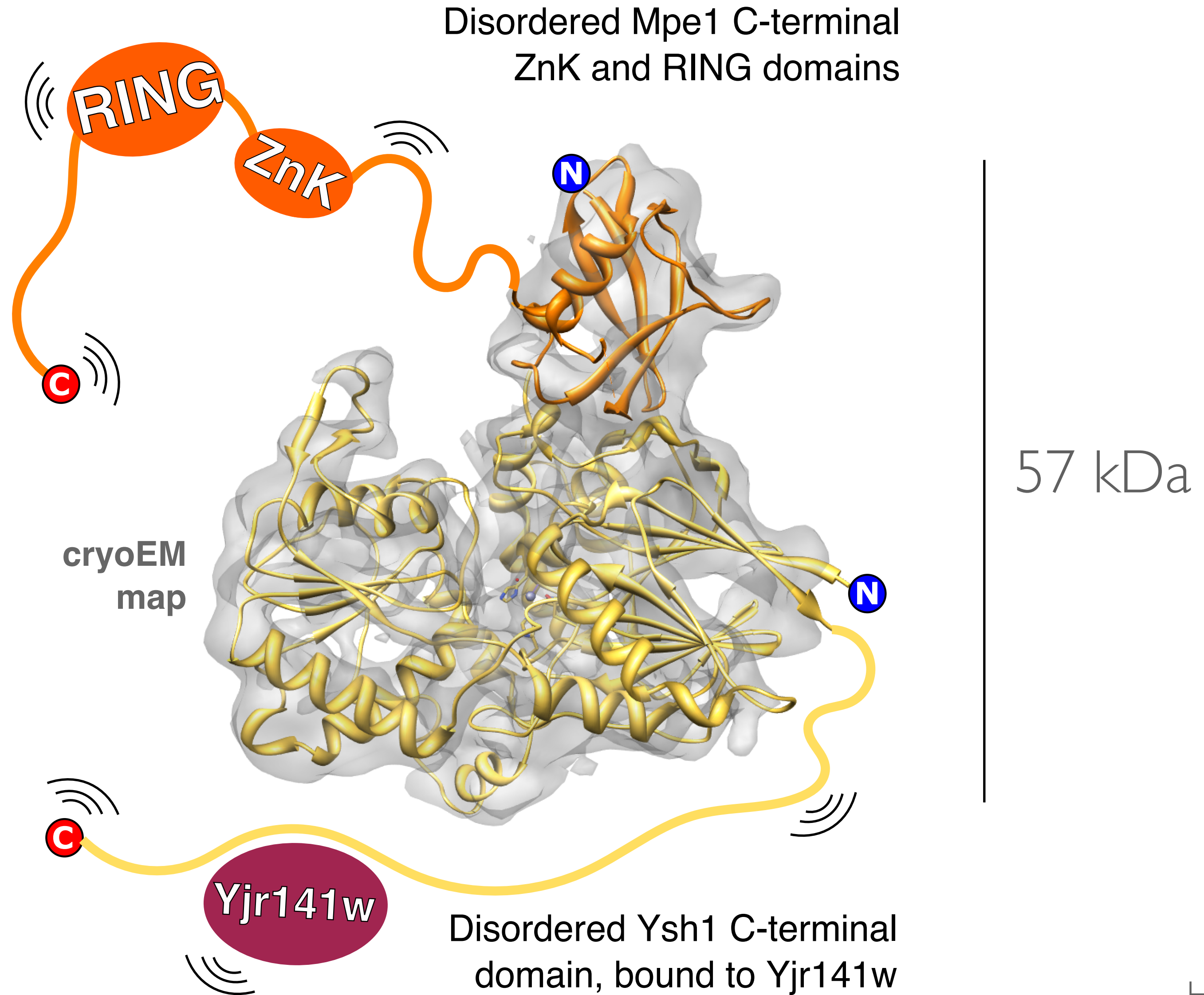
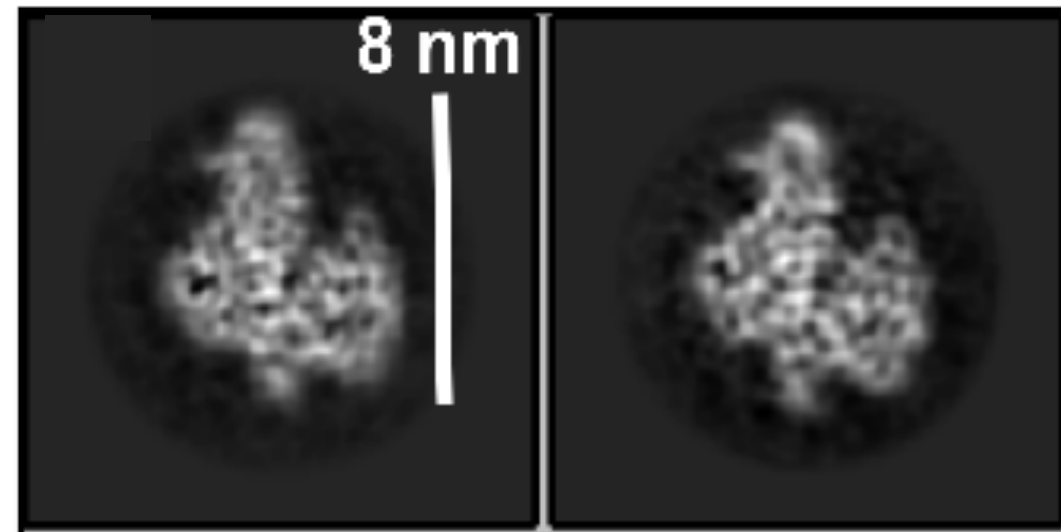
The active site is located
at the end of a long tunnel



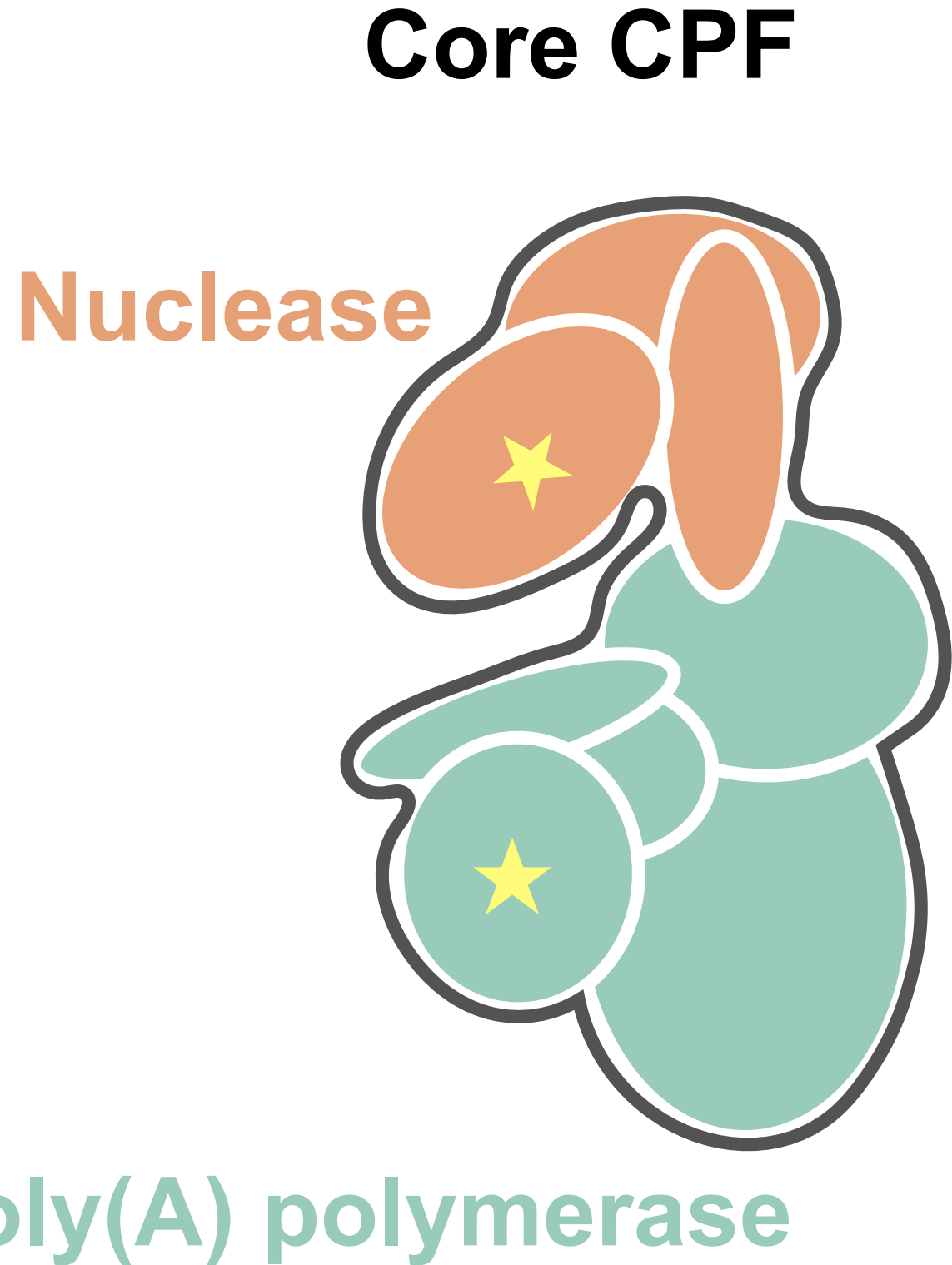
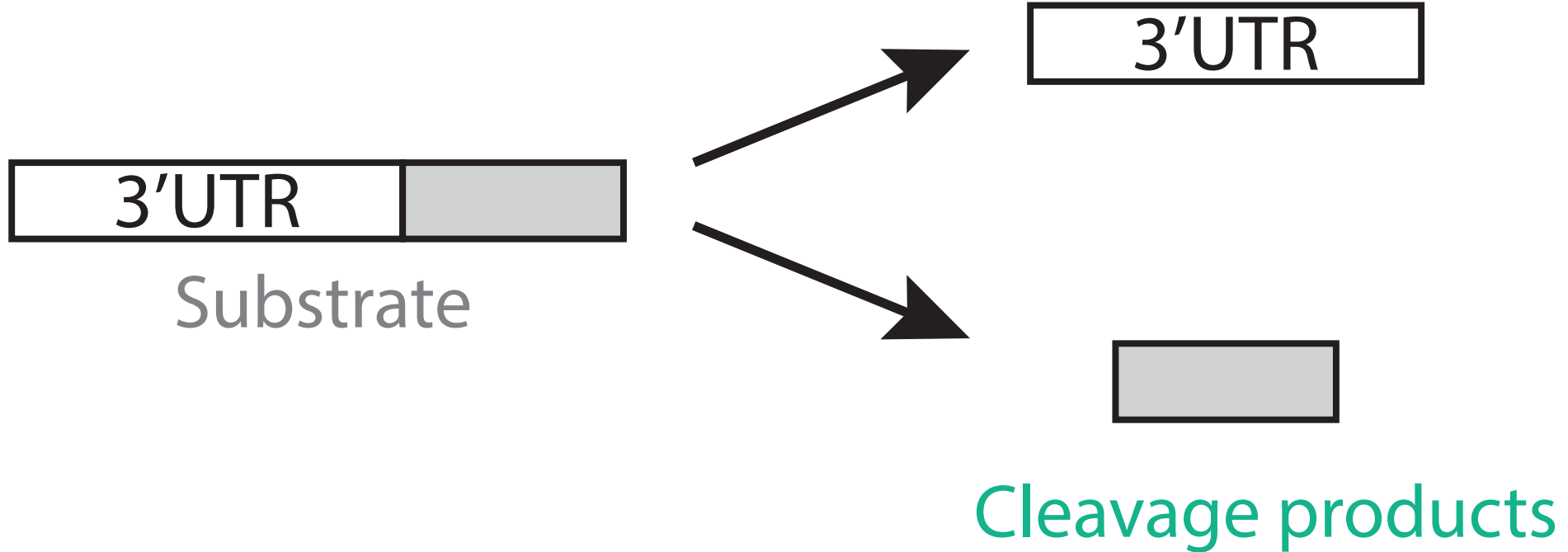
The active site is located
at the end of a long tunnel



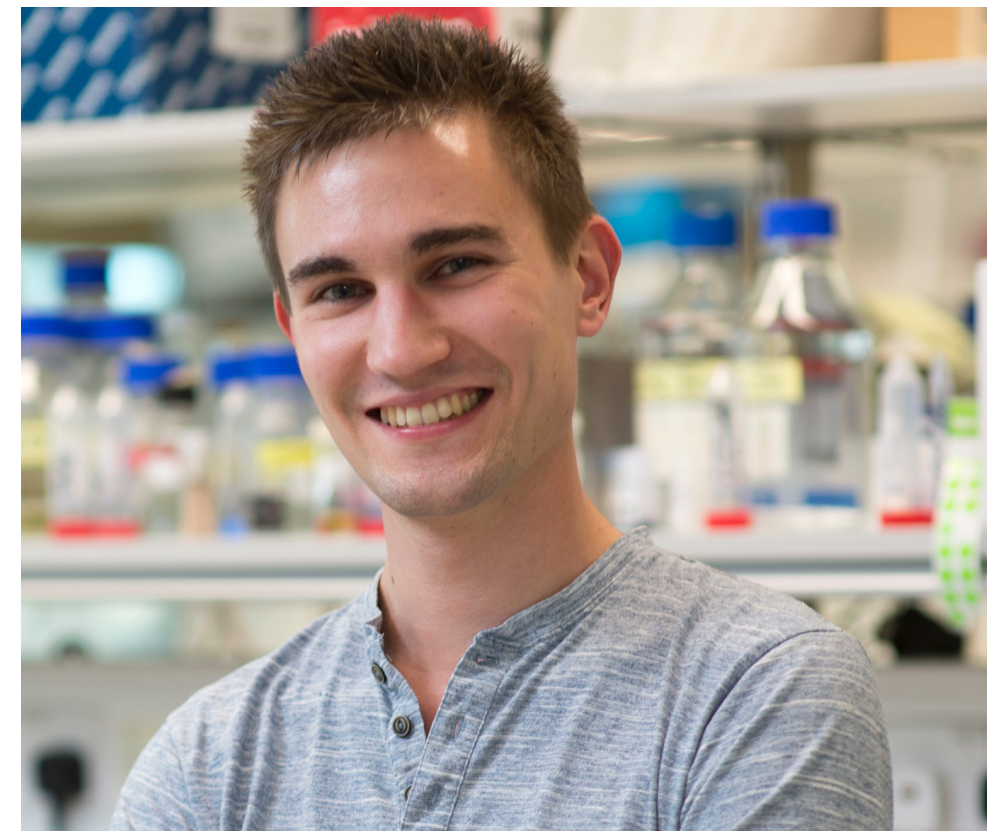
Cryo-EM of Ysh1-Mpe1-Ipa1 complex



Reconstitution of cleavage activity by the Ysh I nuclease

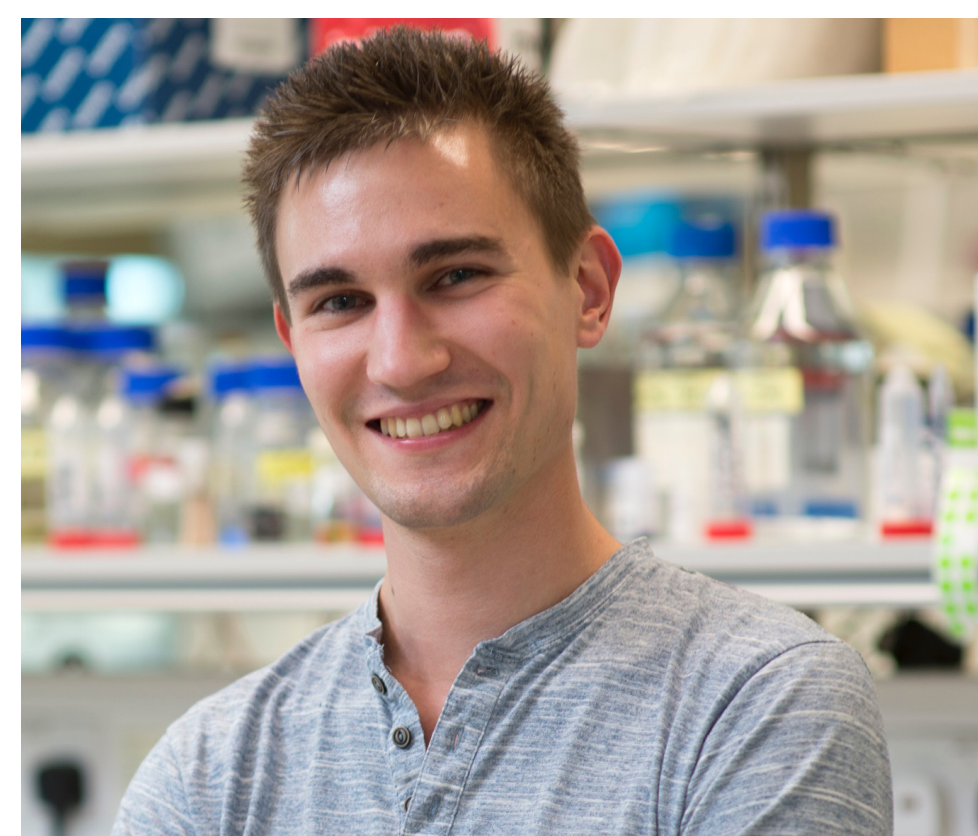
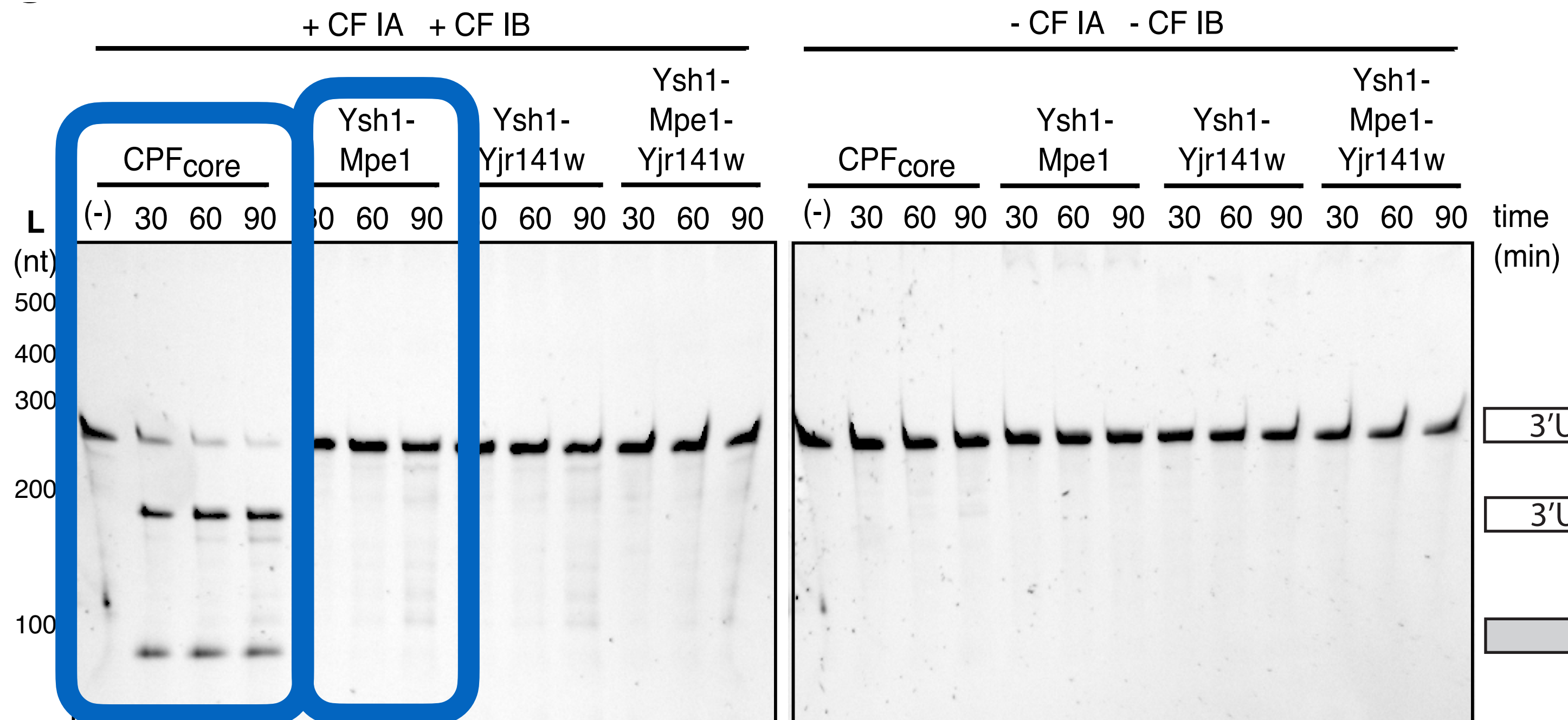
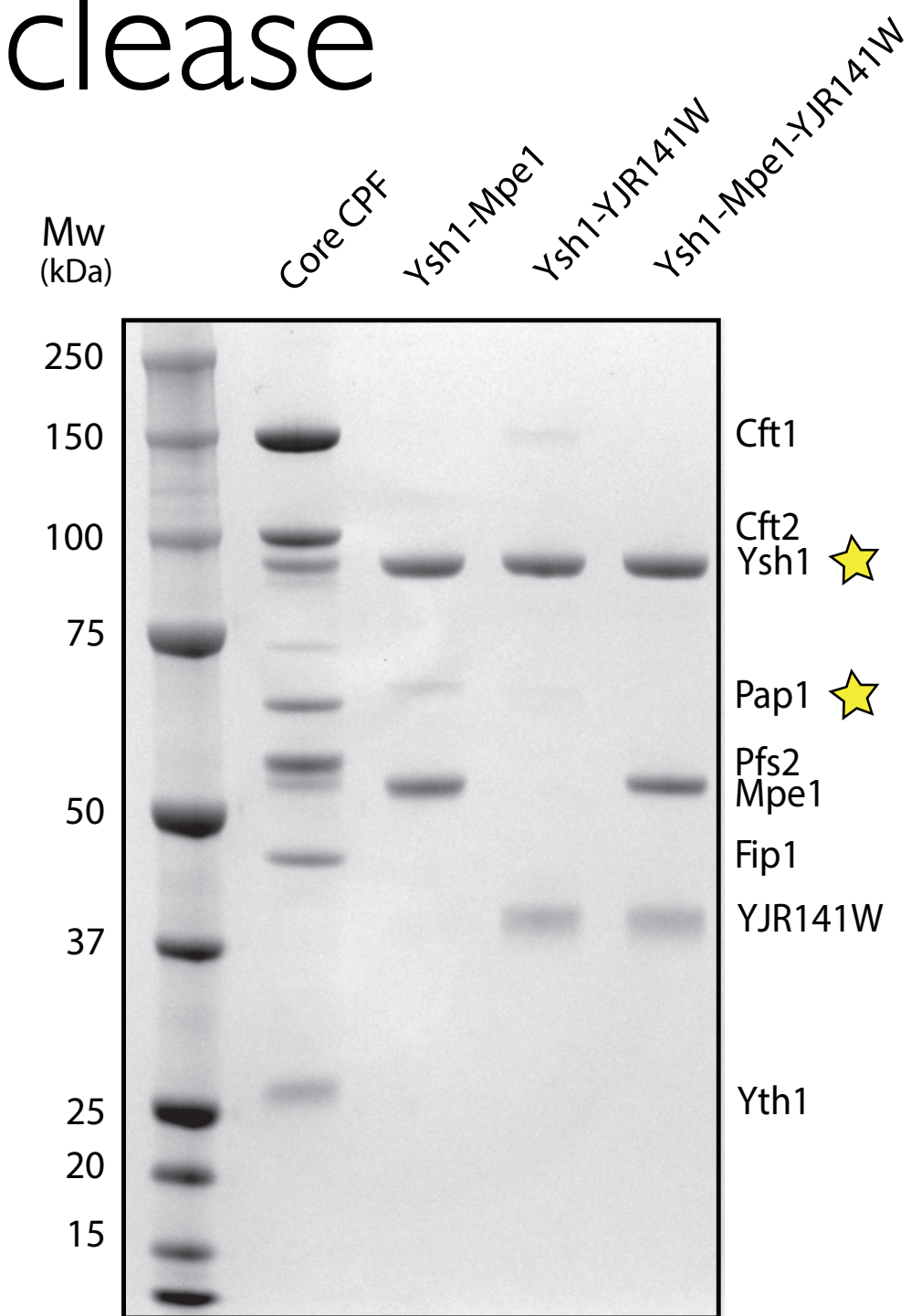
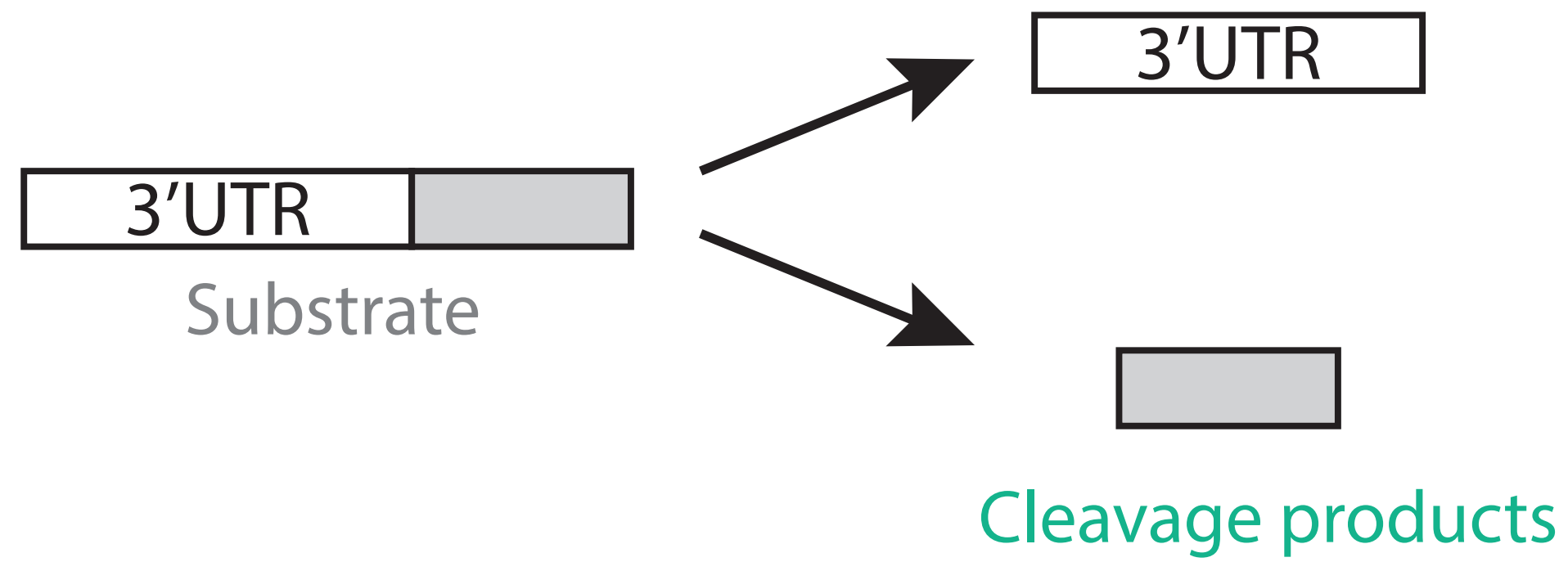


Accessory factors CF IA and CF IB also proposed to play a role in 3' end processing



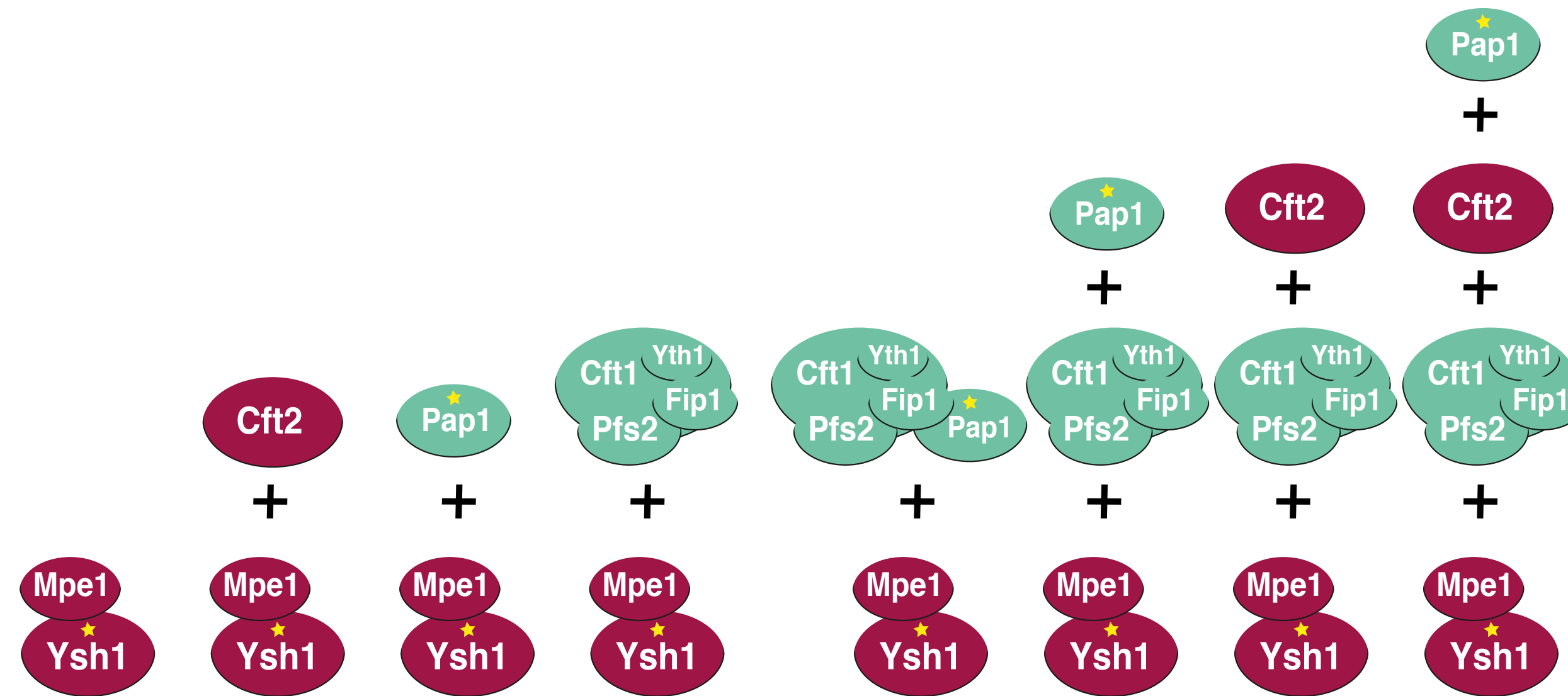
Chris Hill

Reconstitution of cleavage activity by the Ysh I nuclease



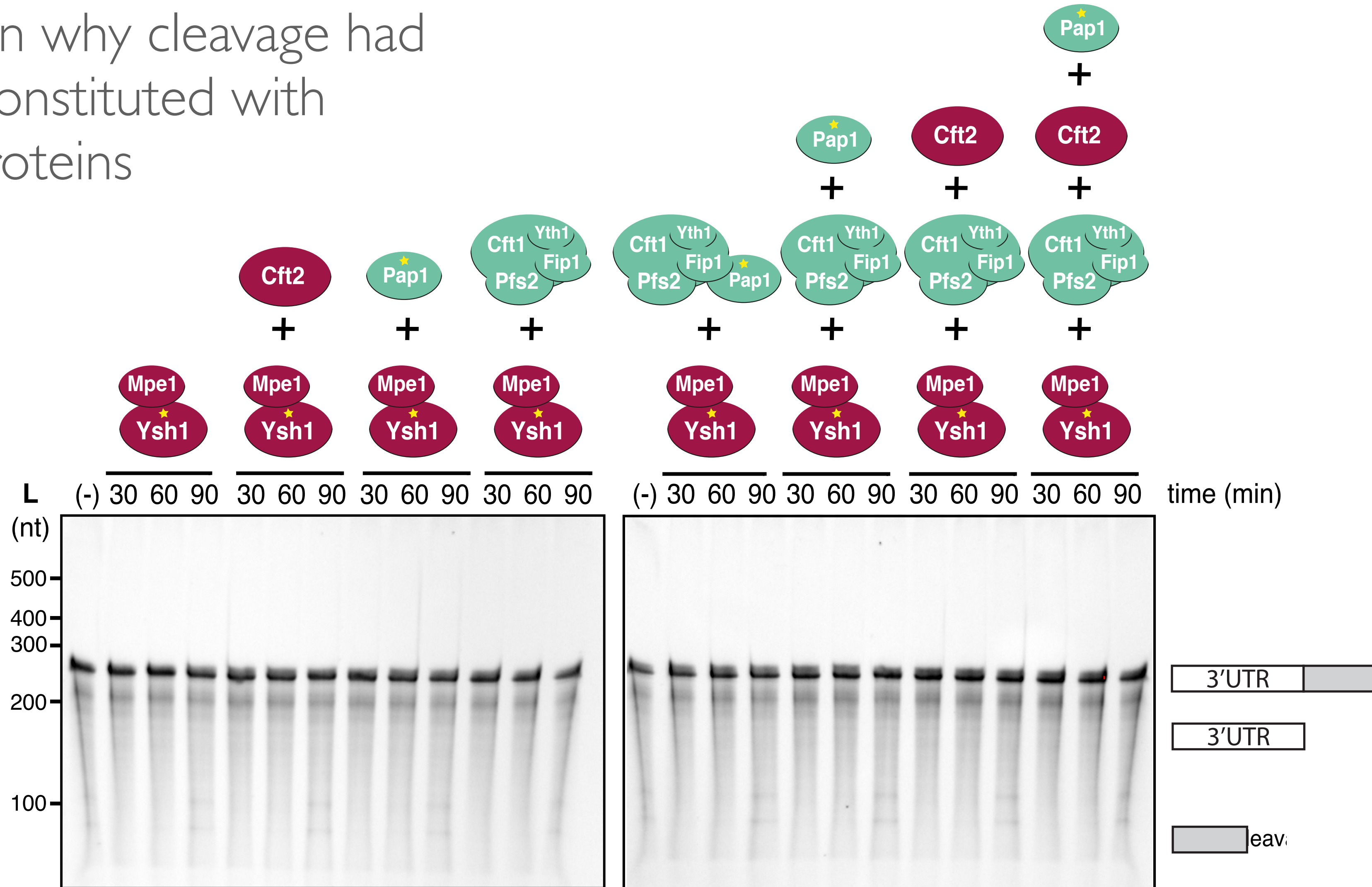
Chris Hill

Reconstitution of cleavage activity

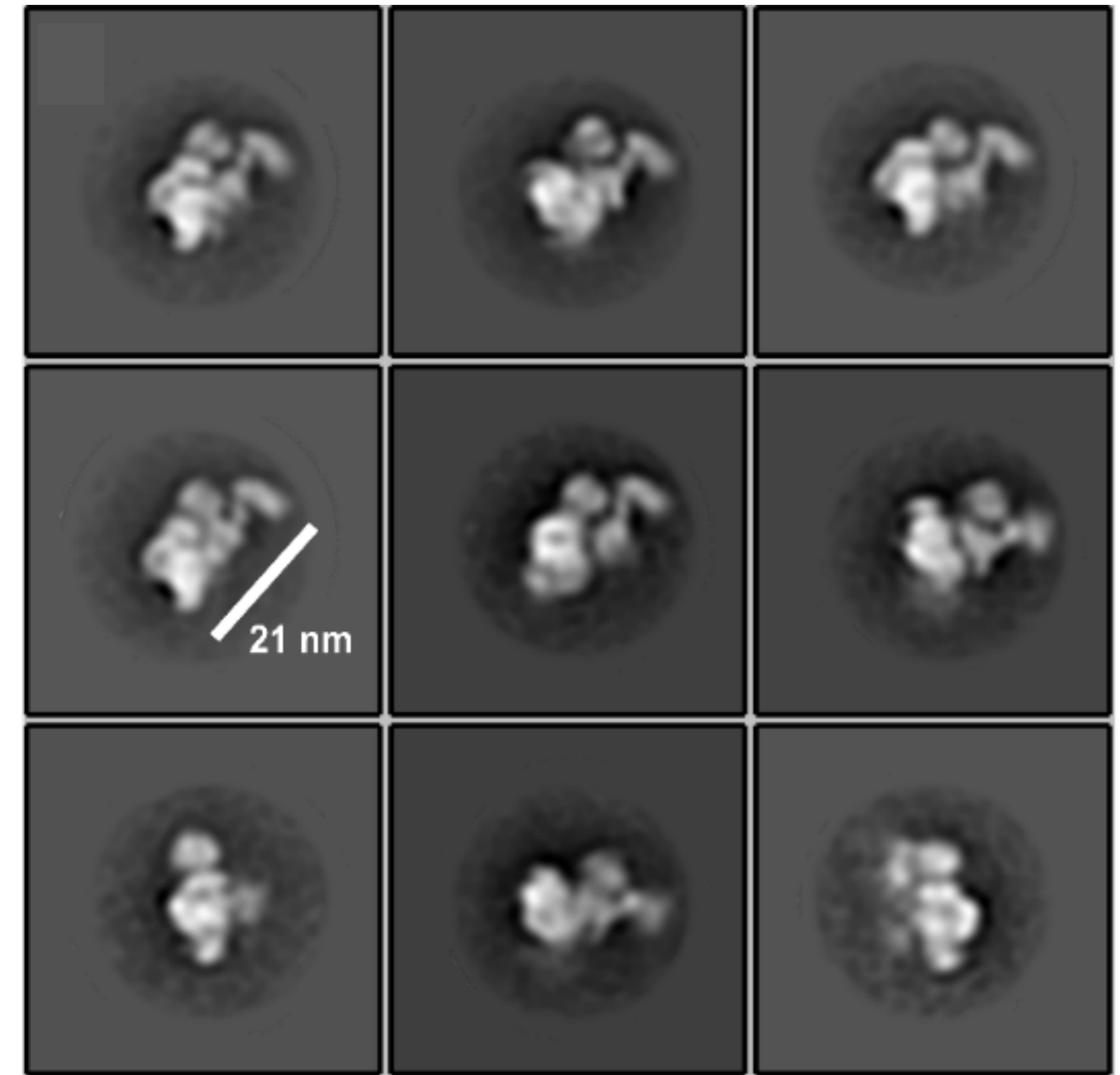
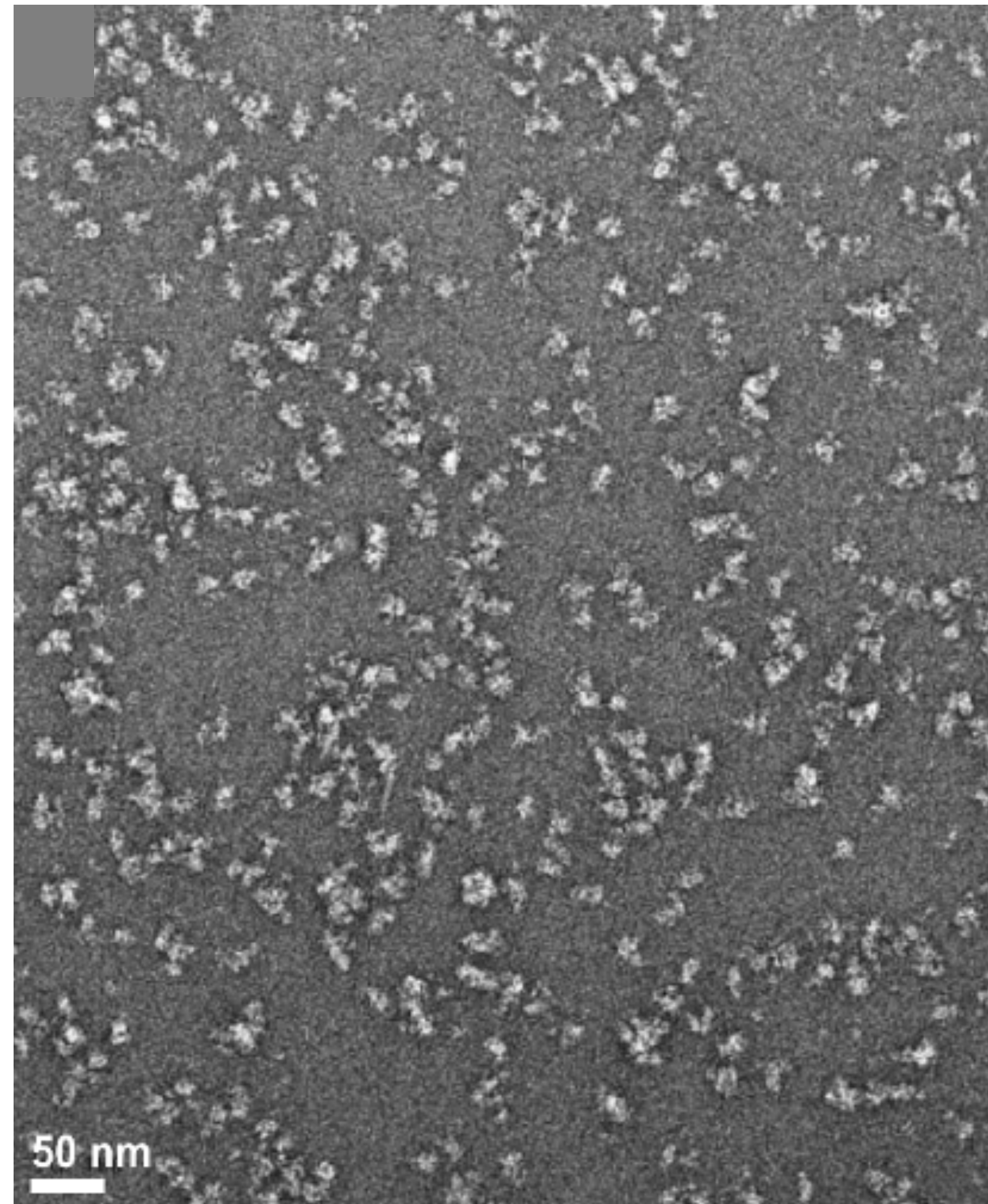
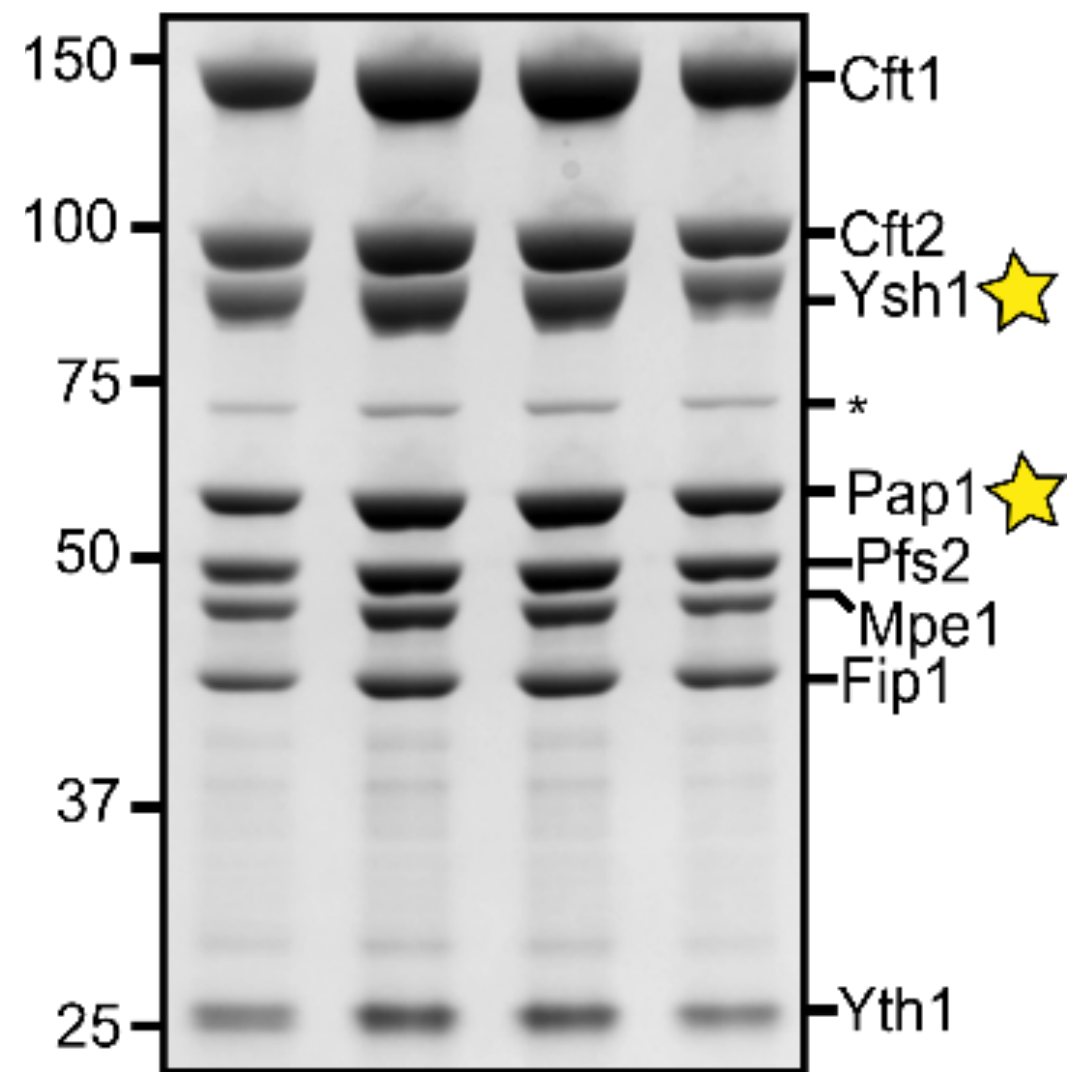


Reconstitution of cleavage activity

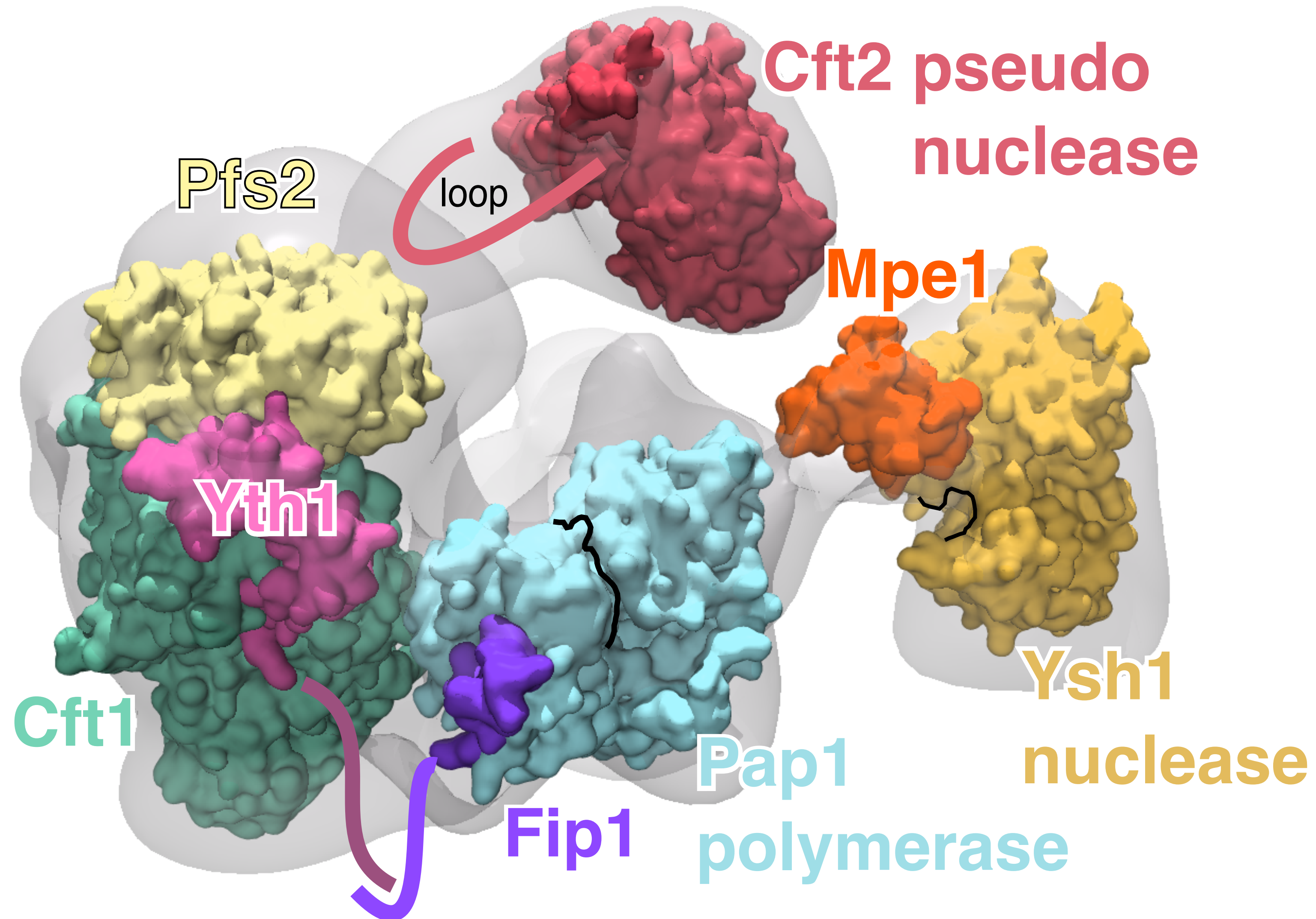
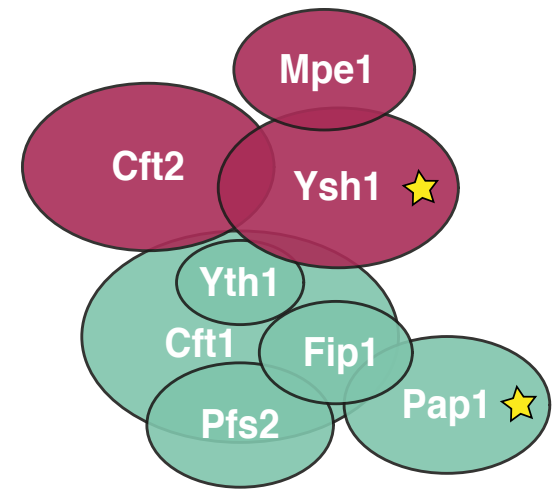
This may explain why cleavage had never been reconstituted with recombinant proteins



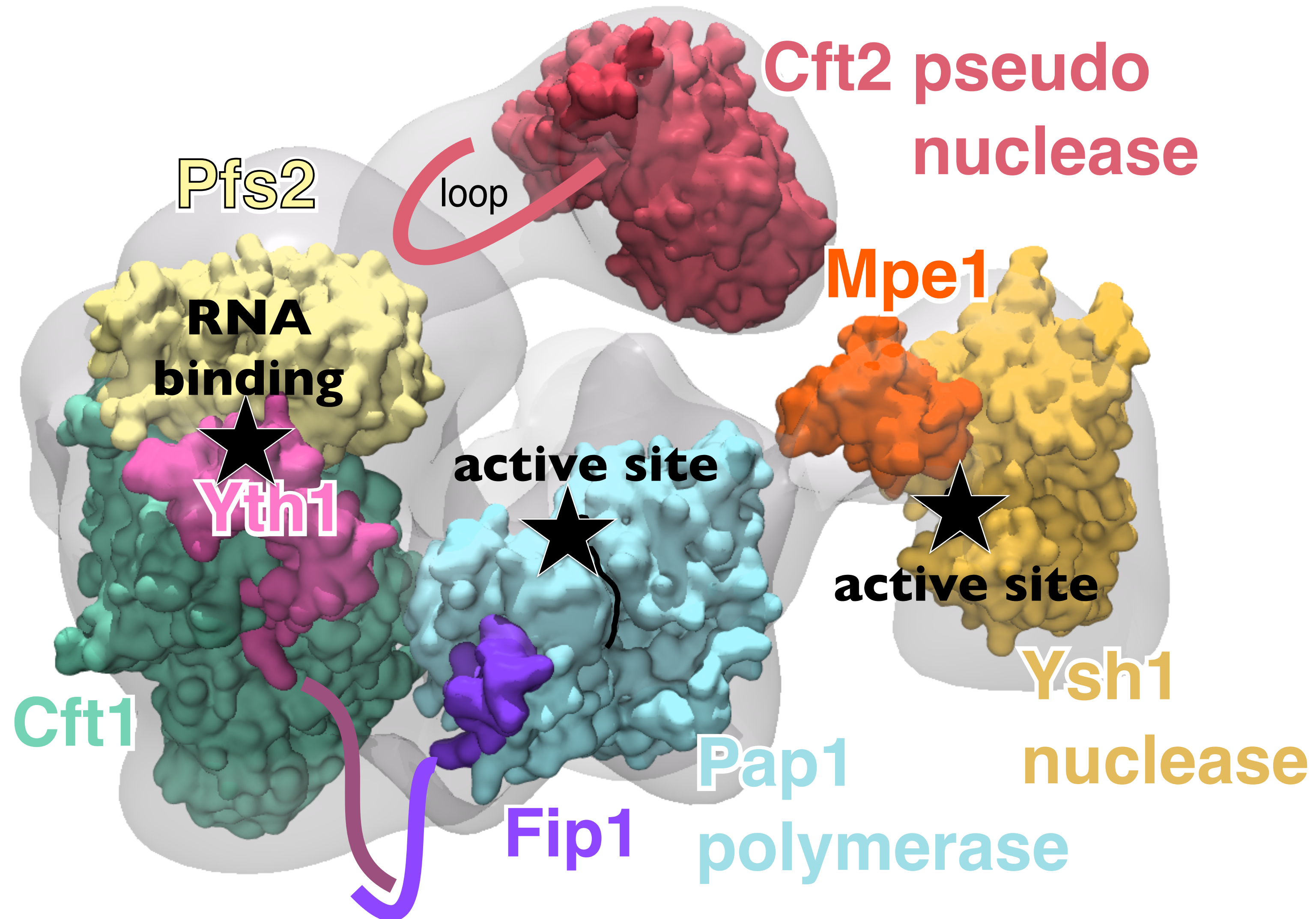
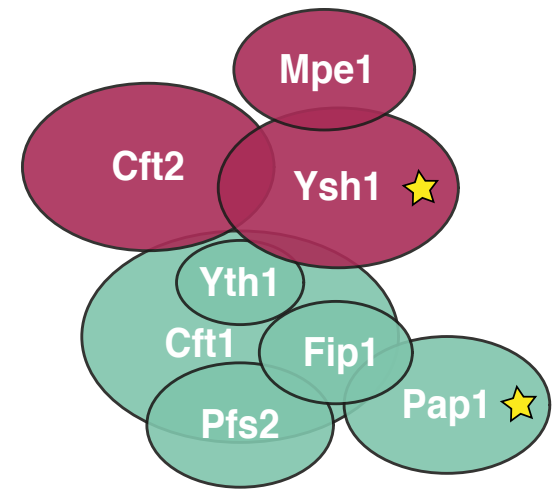
Negative Stain EM of Core CPF



Architecture of core CPF

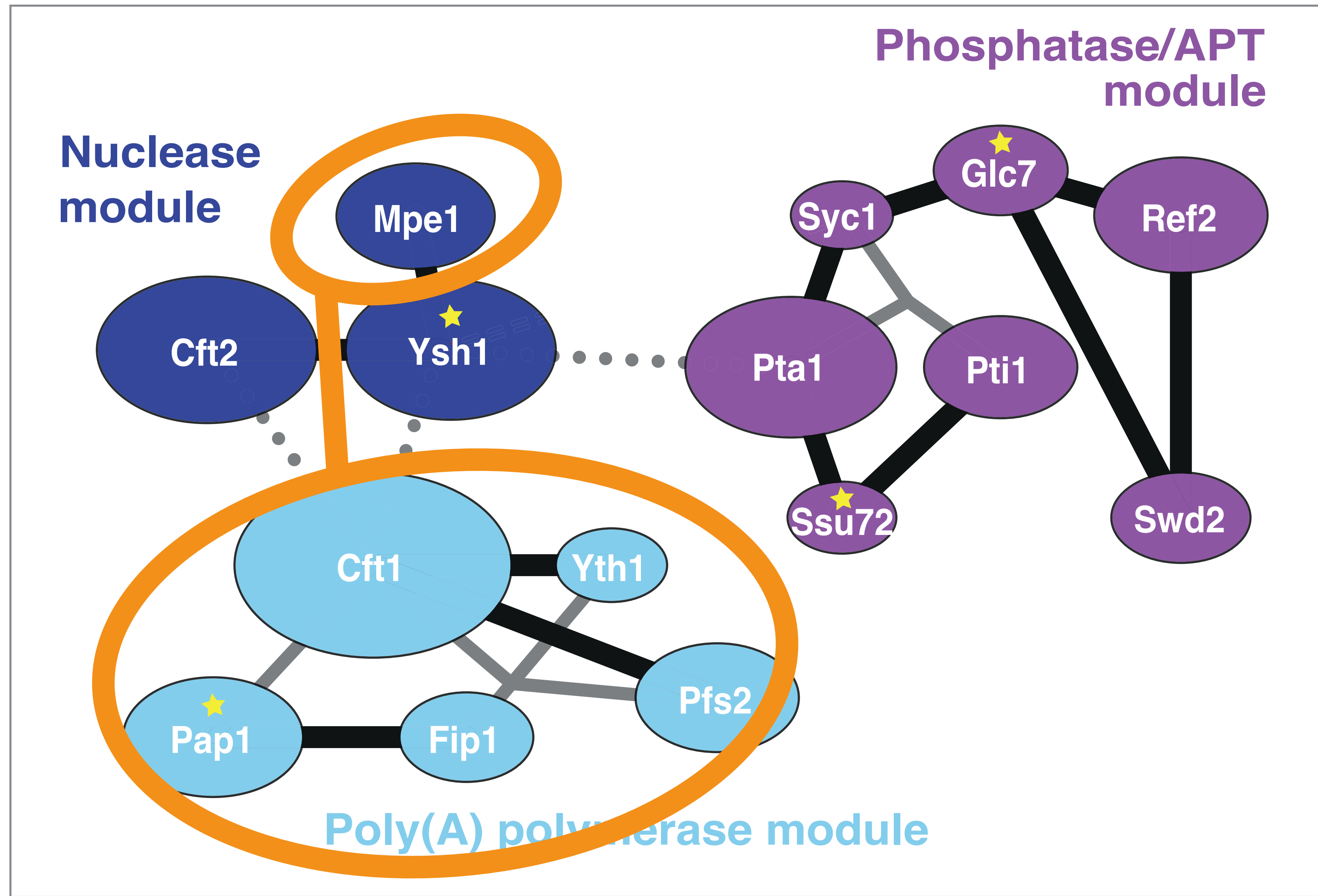


Architecture of core CPF



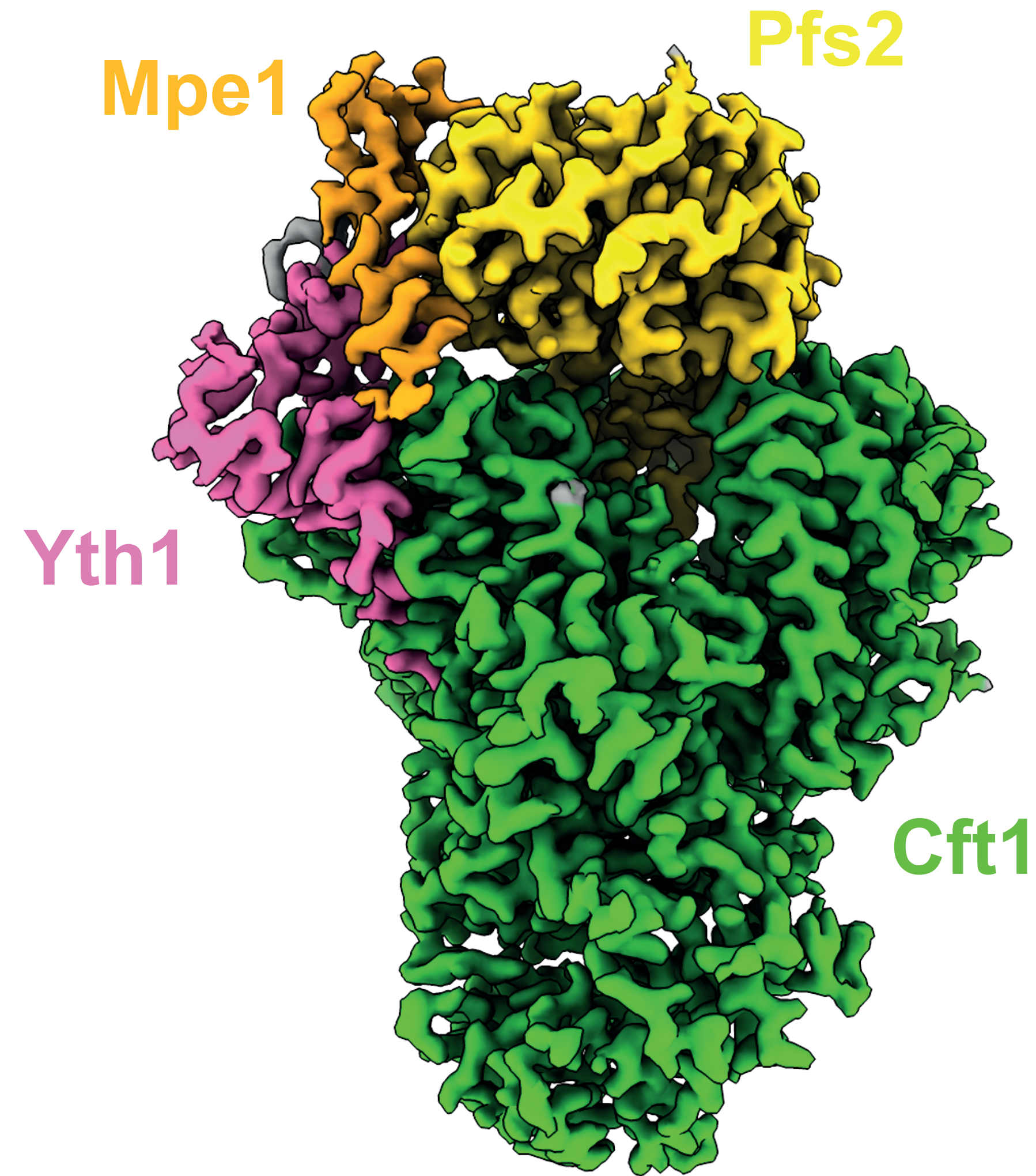


Juan Rodriguez-Molina



Vo et al 2001
Di Giammartino et al 2014
Lee and Moore 2014
Baejen et al 2014

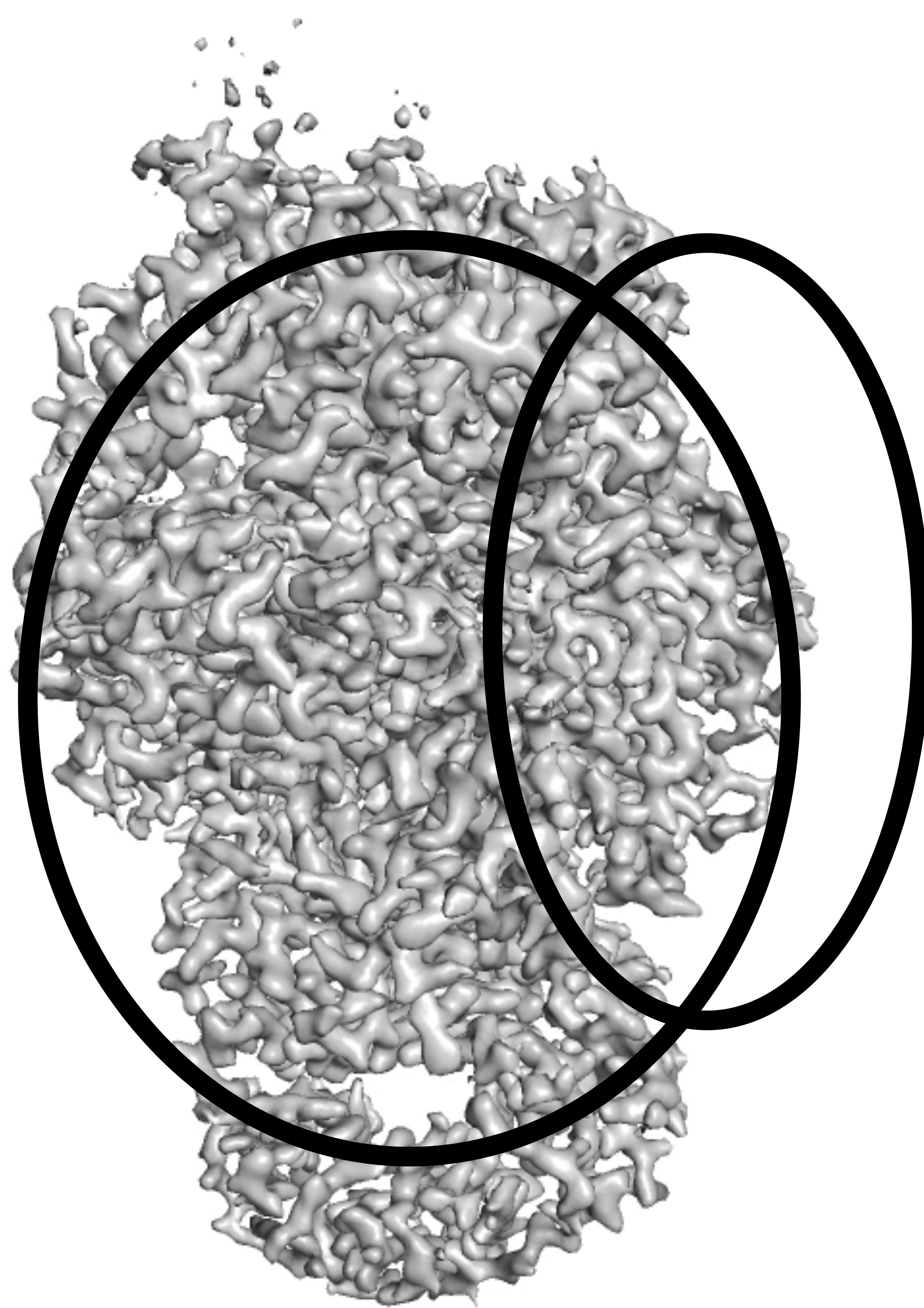
Mpe1 binds the polymerase module



2.7 Å resolution

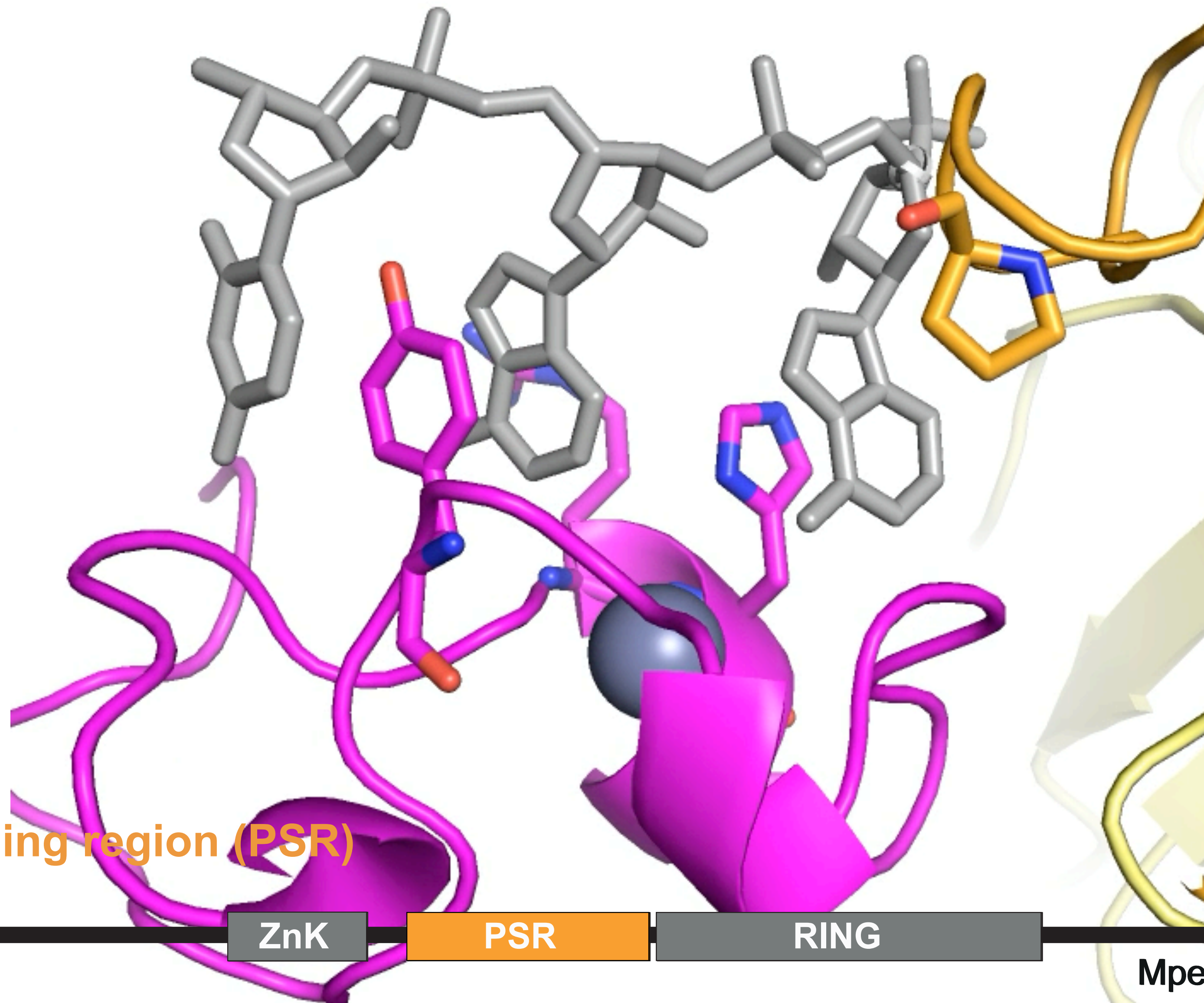
Rodriguez-Mollina et al
Mol Cell 2022

RNA



Mpe1

Yth1



pre-mRNA sensing region (PSR)

UBL

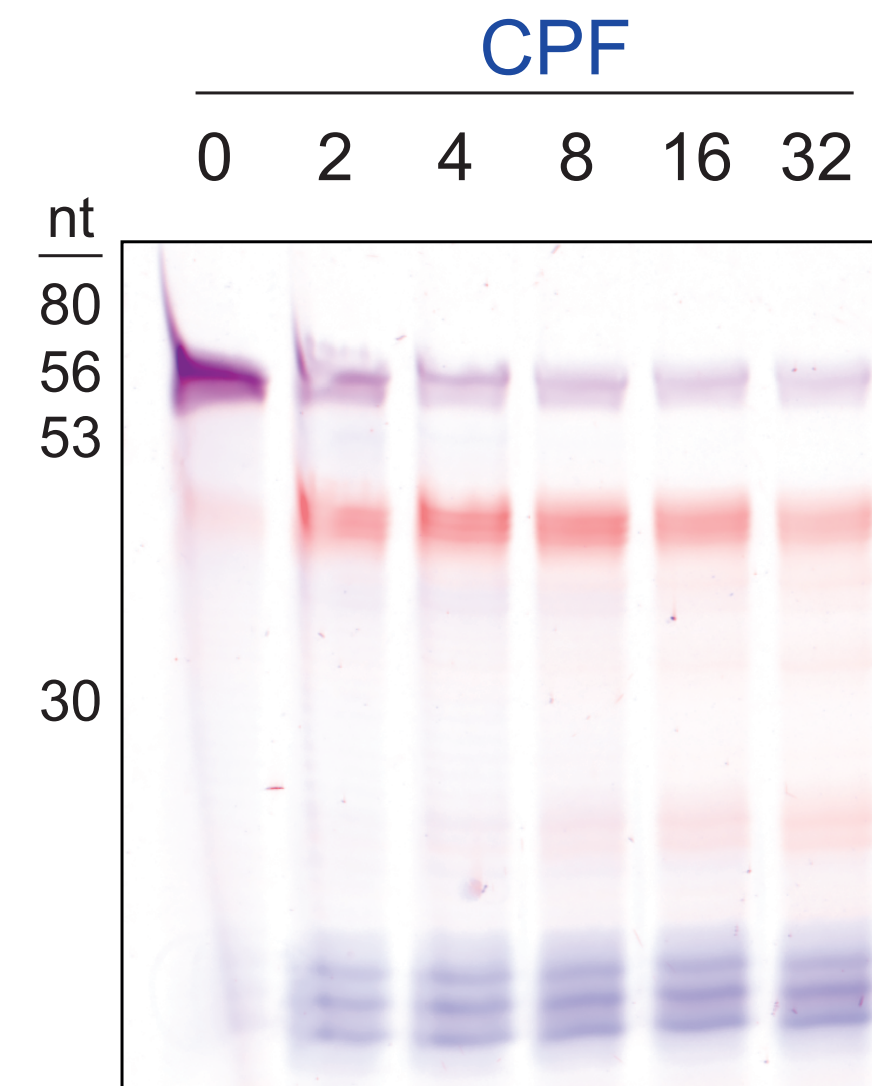
ZnK

PSR

RING

Mpe1, 441 aa

Mpe1 is important for cleavage



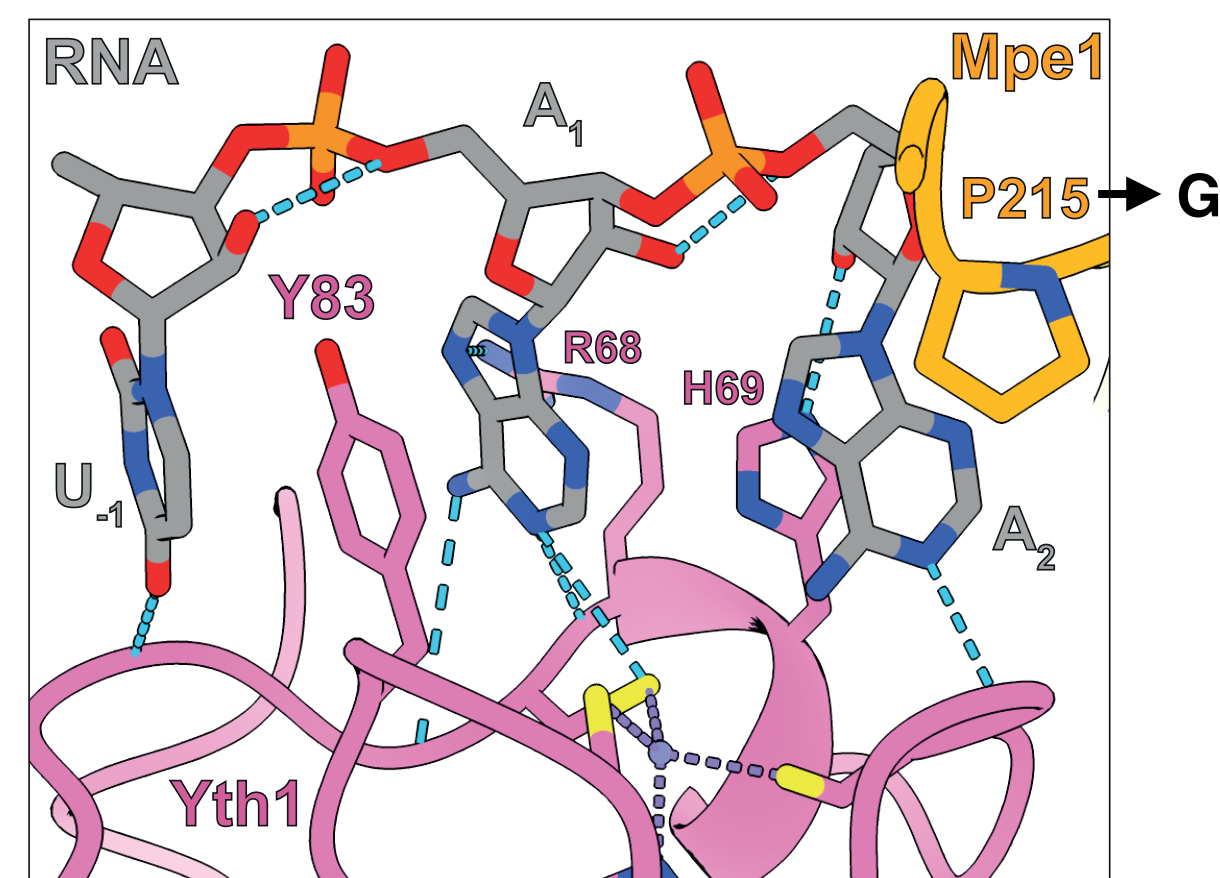
min



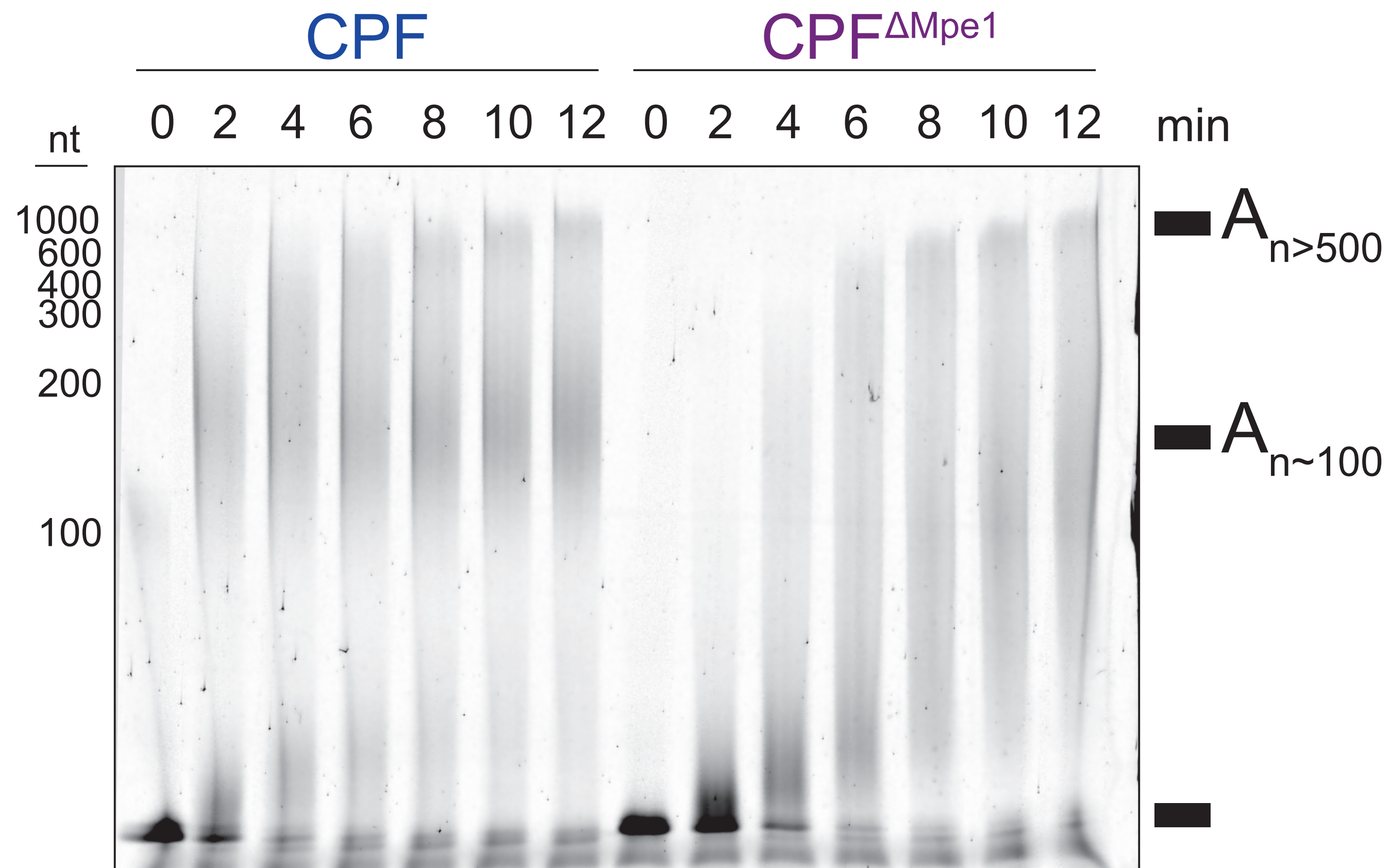
5'   3'



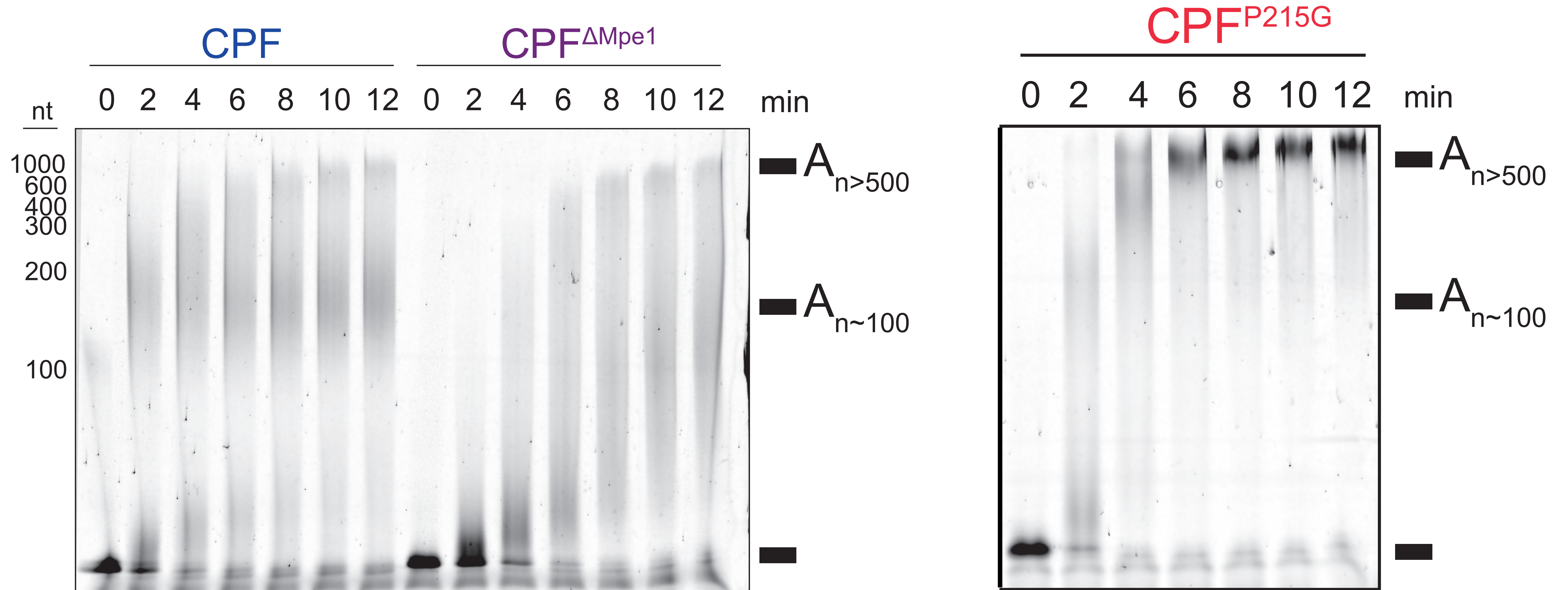
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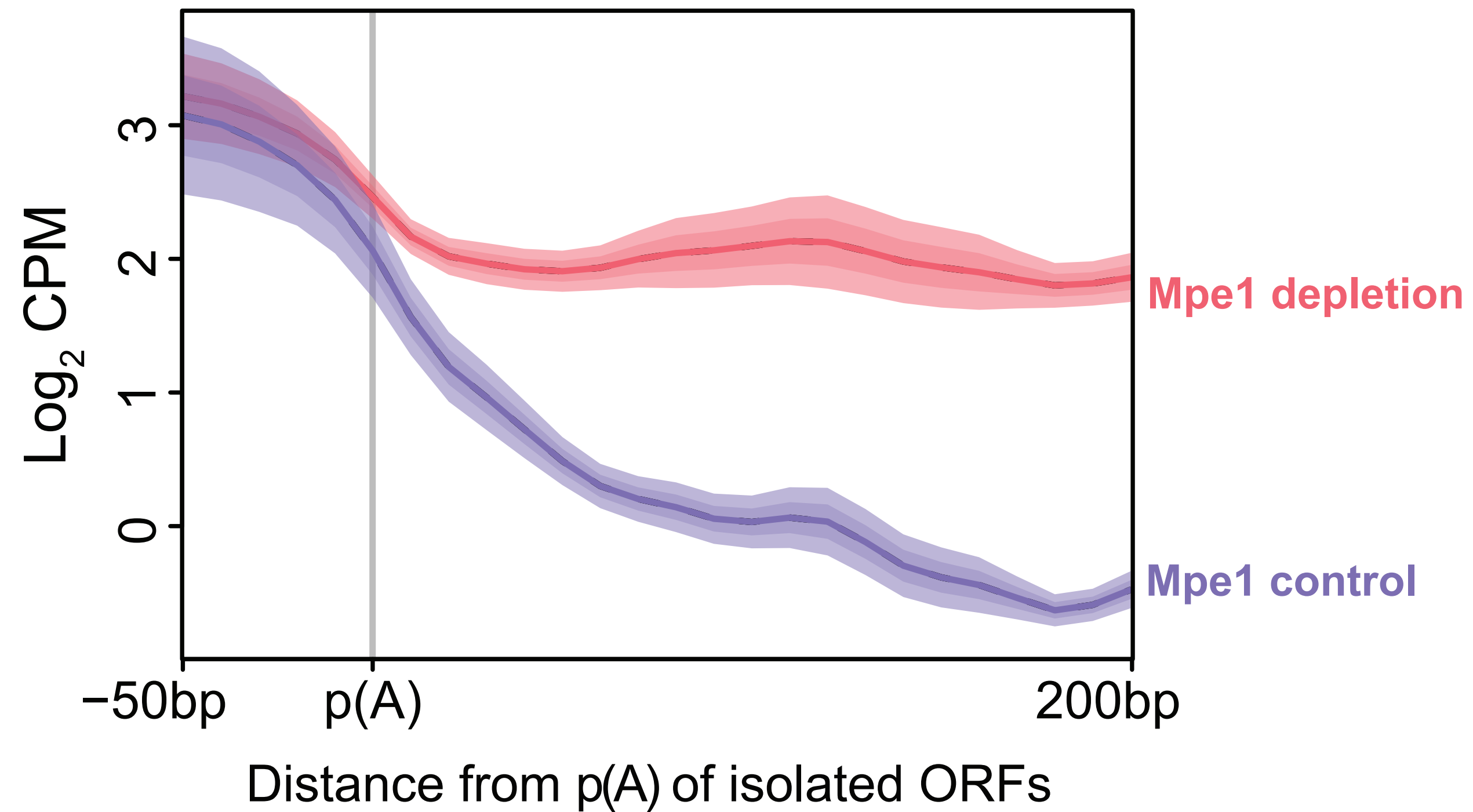
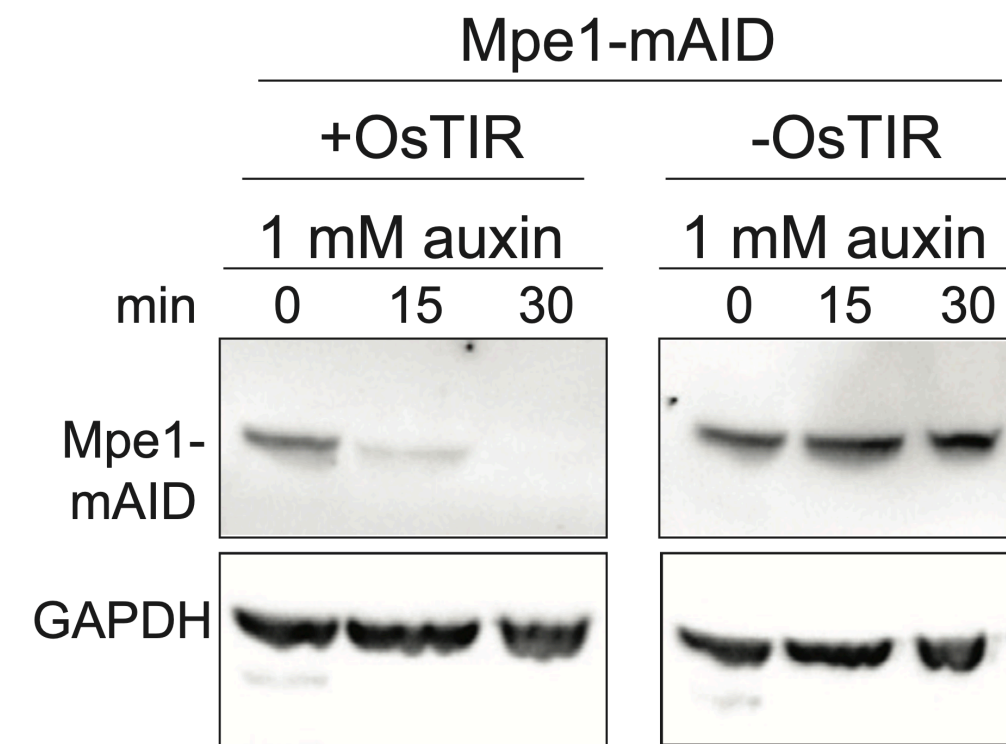
Mpe1 is important for cleavage and polyadenylation



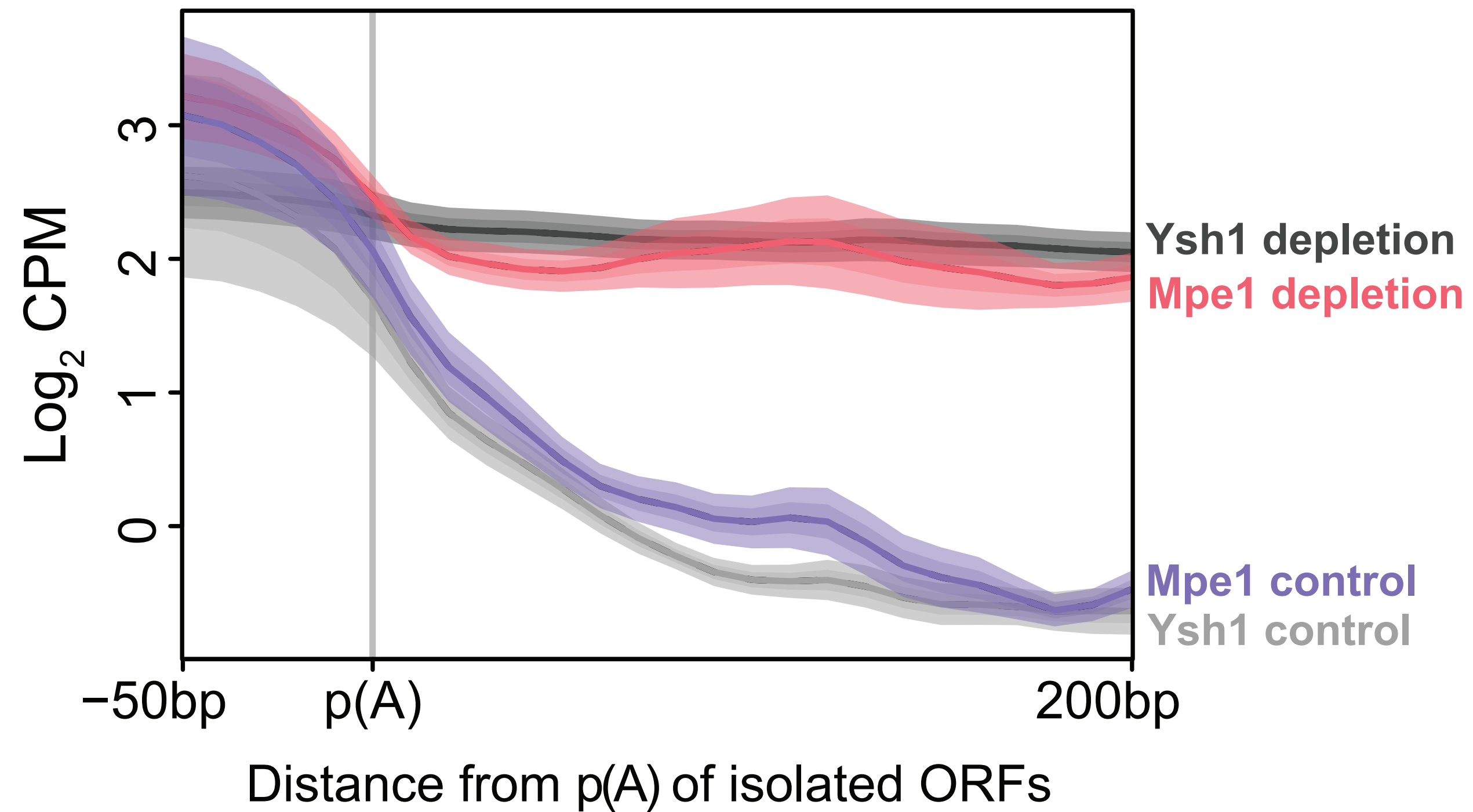
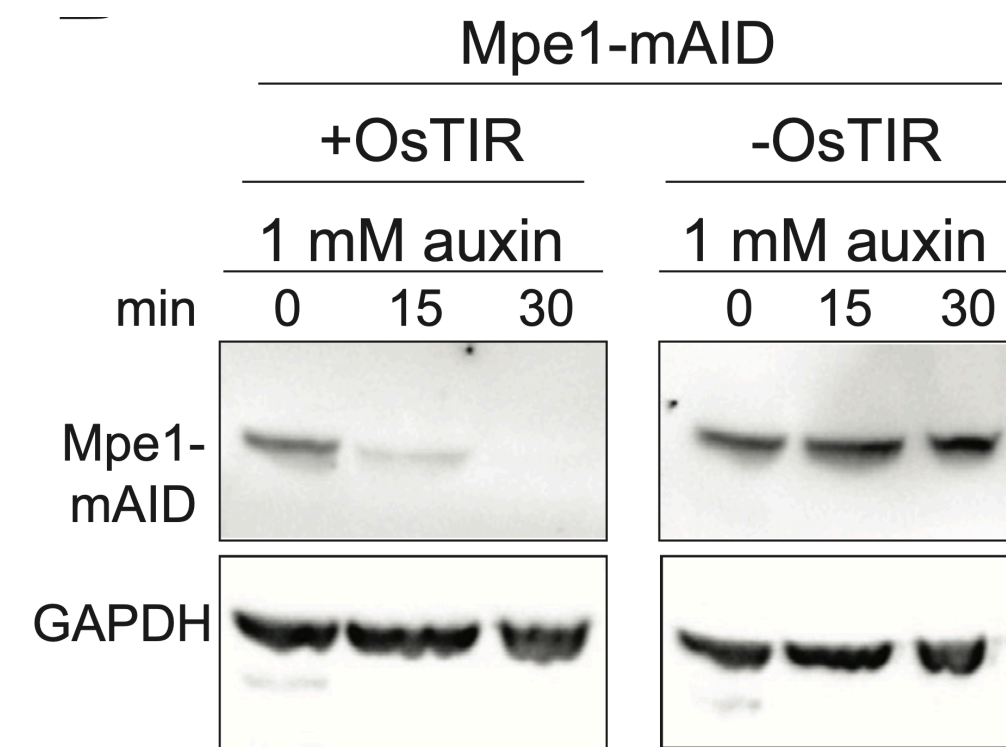
Mpe1 is important for cleavage and polyadenylation



Mpe1 is required for transcription termination



Mpe1 is required for transcription termination

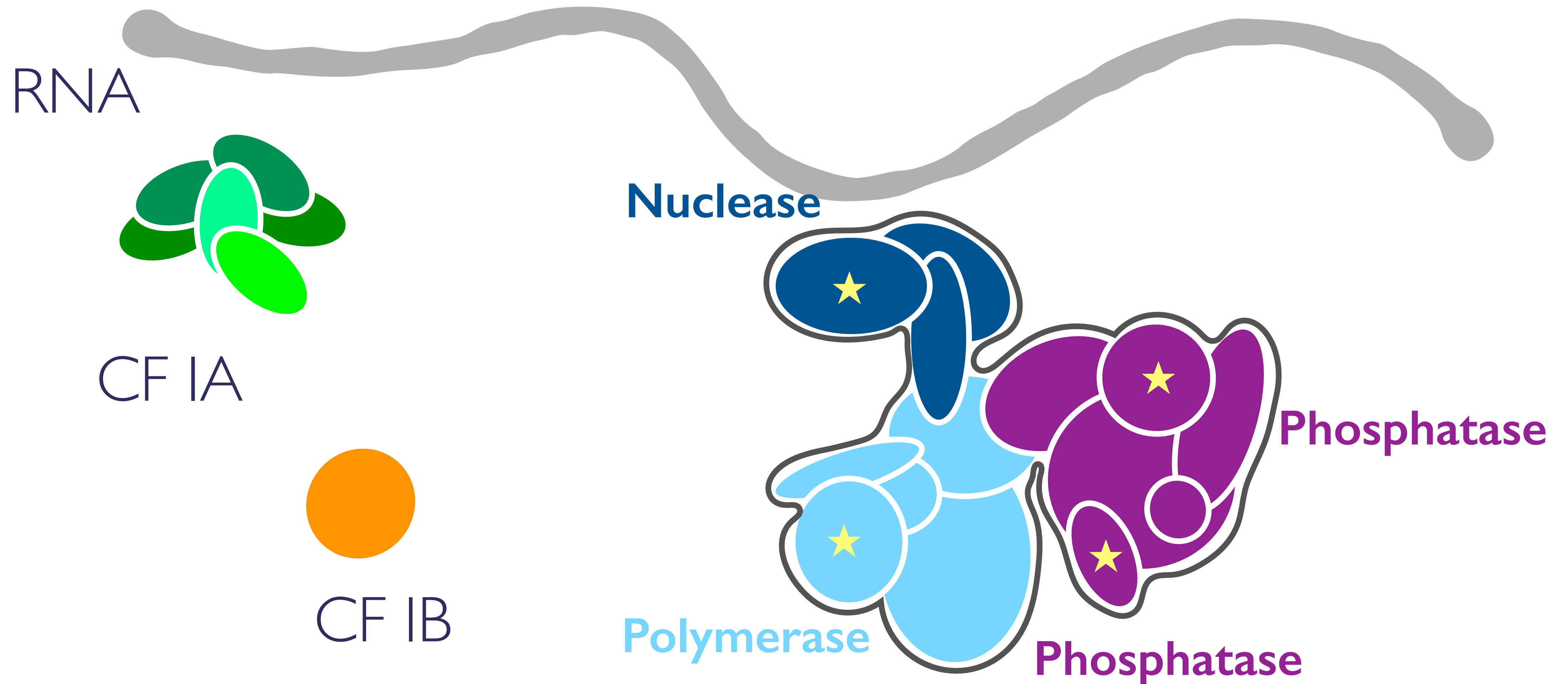


Baejen et al 2017

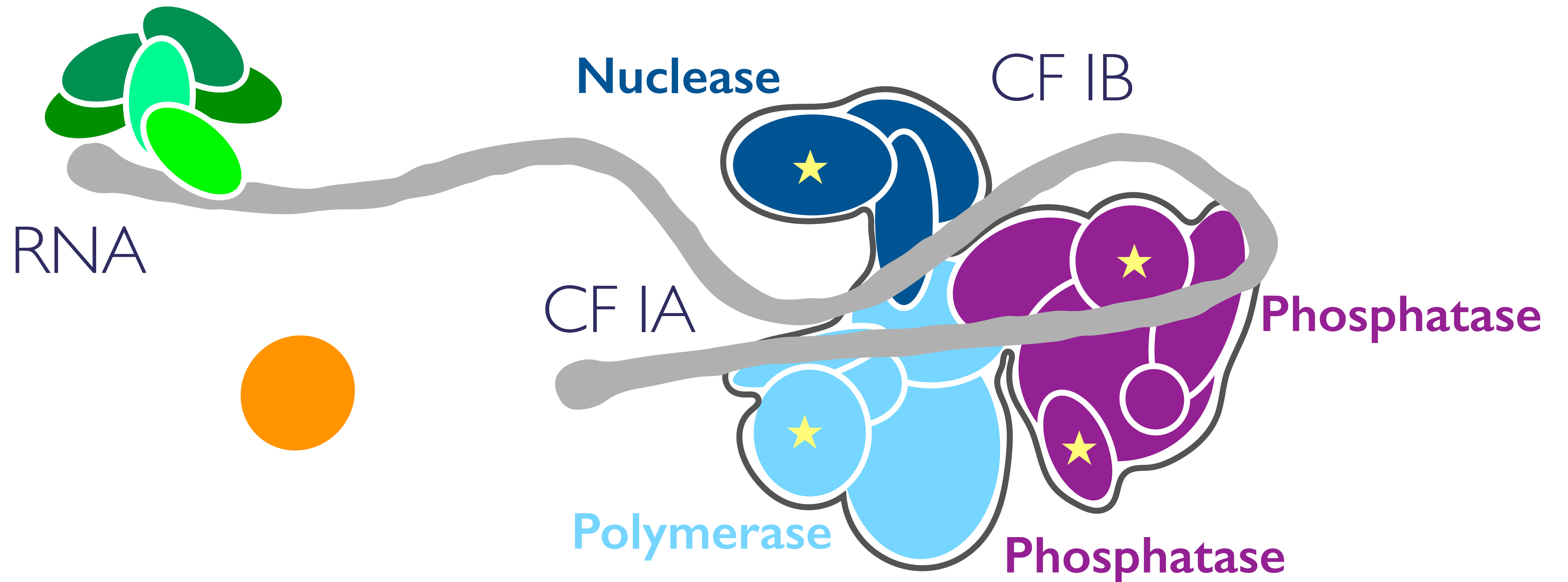
Rodriguez-Mollina et al
Mol Cell 2022

**Dynamics likely regulate CPF
activation**

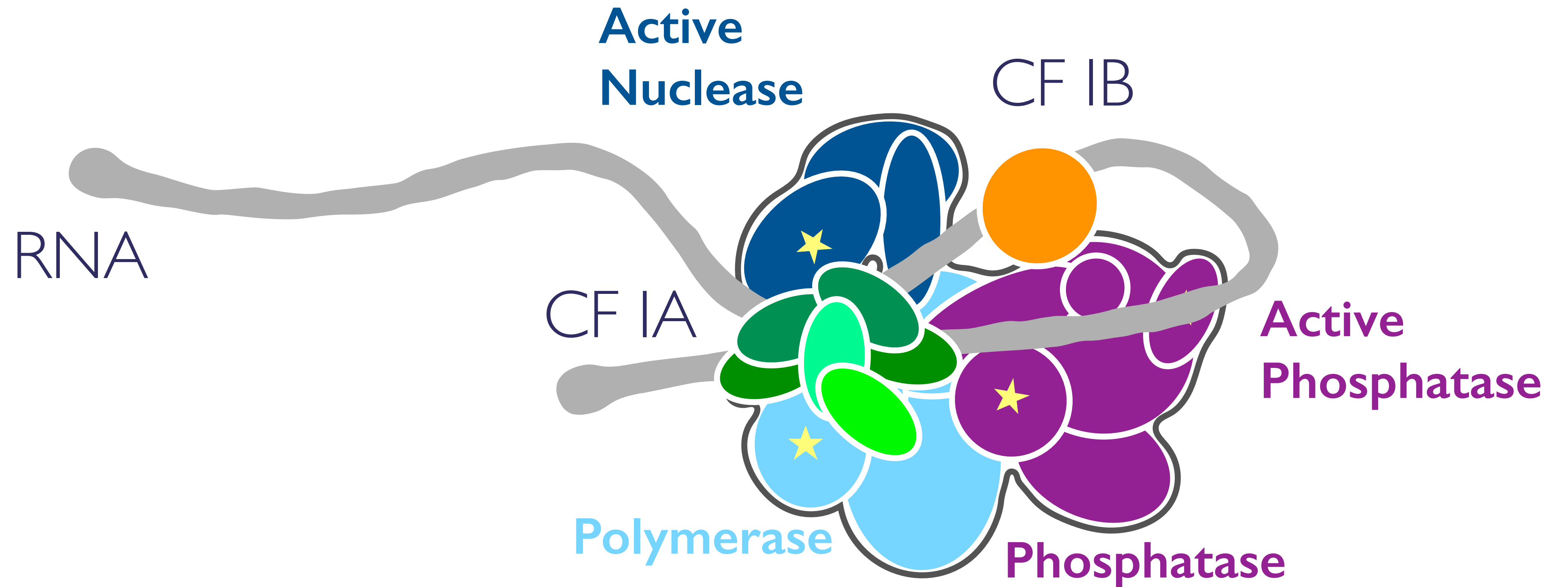
Dynamics likely regulate CPF activation



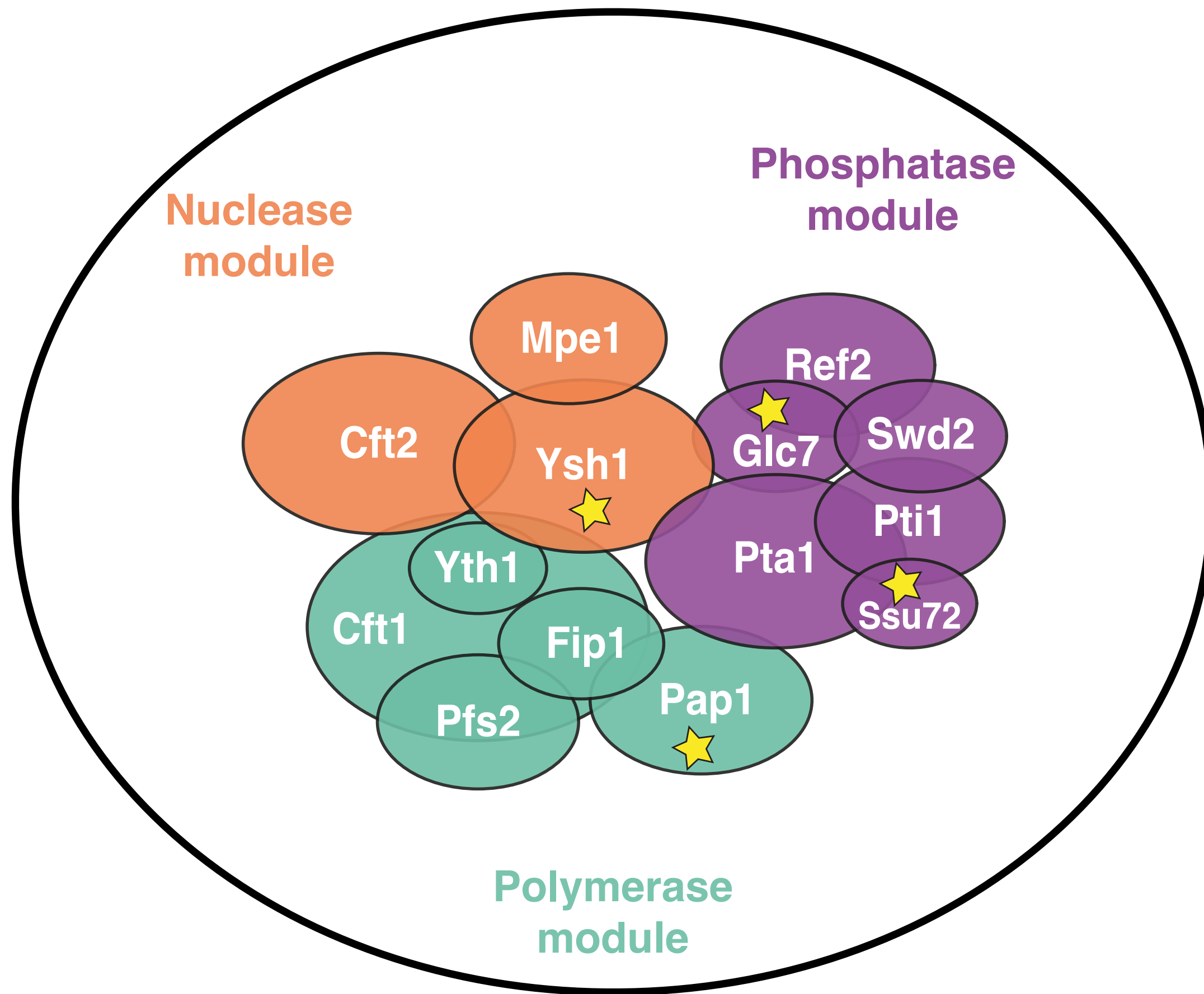
Dynamics likely regulate CPF activation



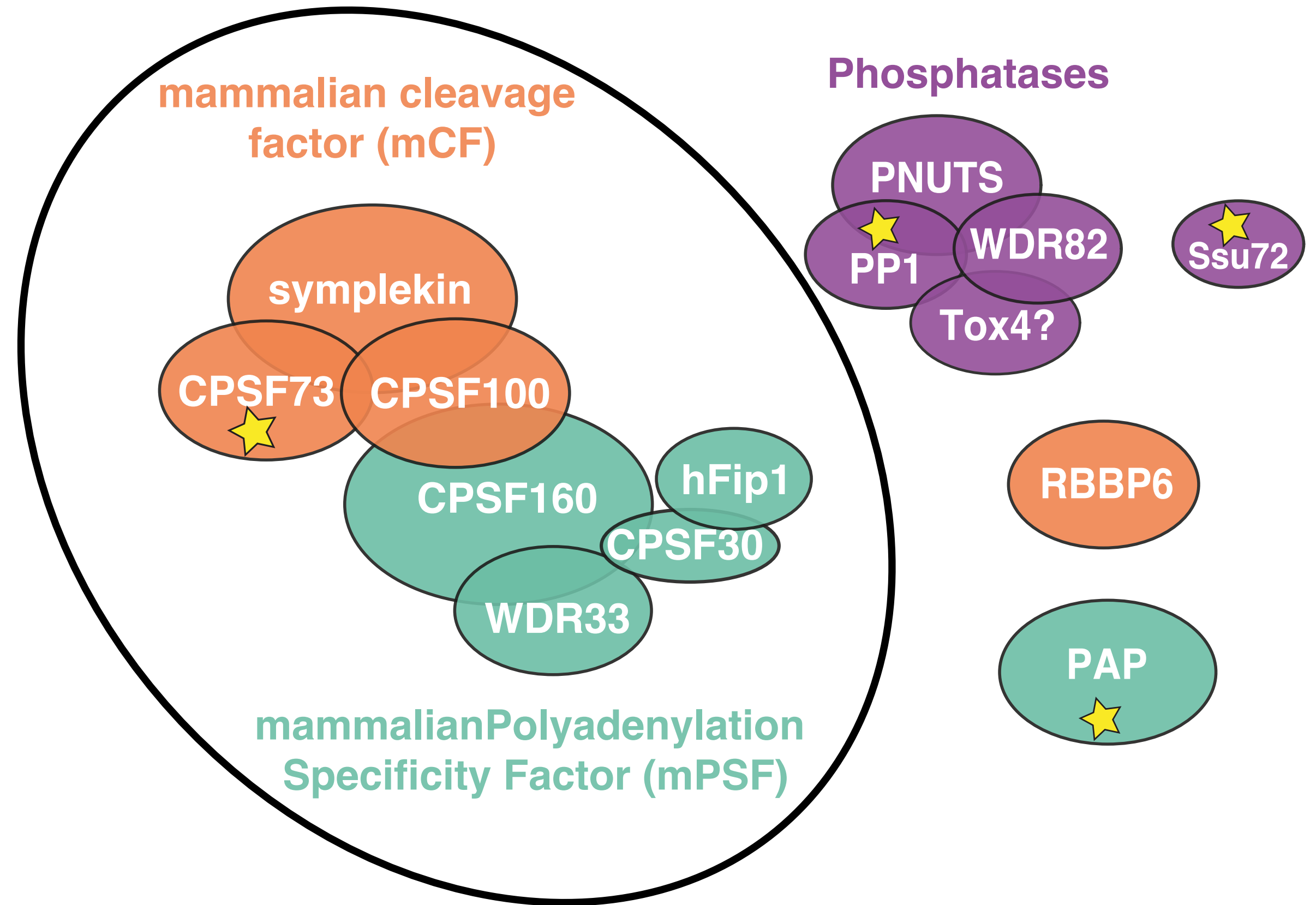
Dynamics likely regulate CPF activation



What about the human complex?

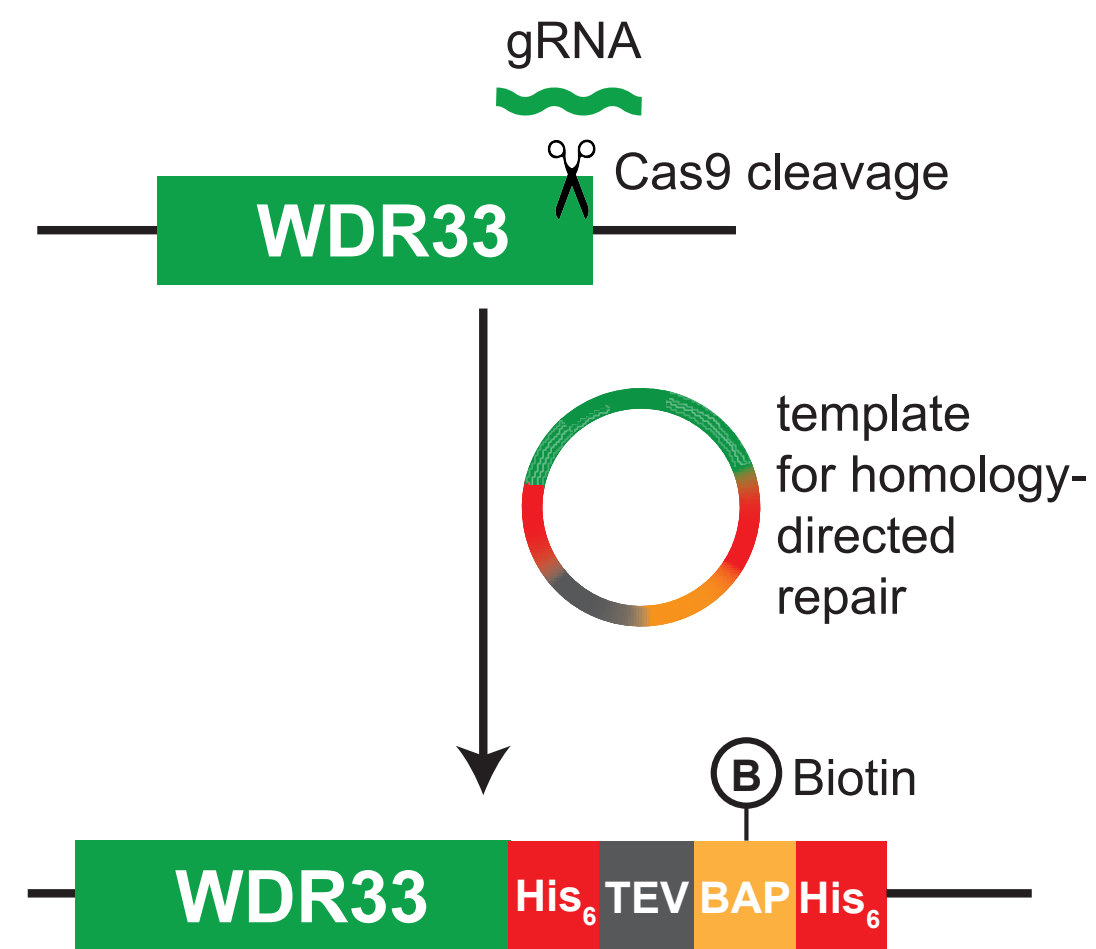


Yeast CPF

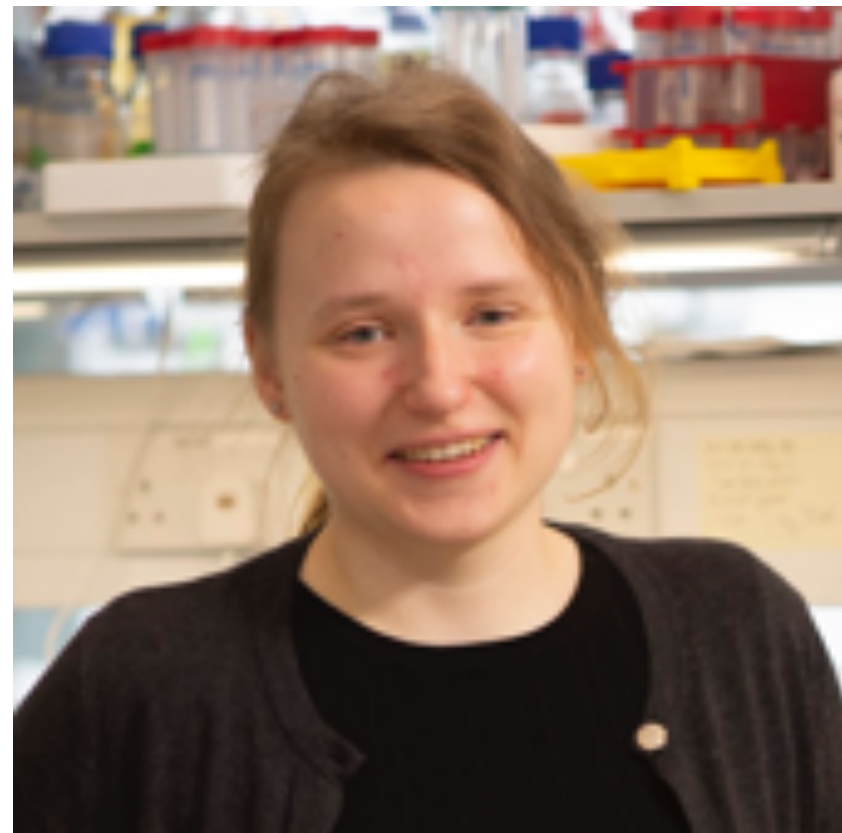


Human CPSF

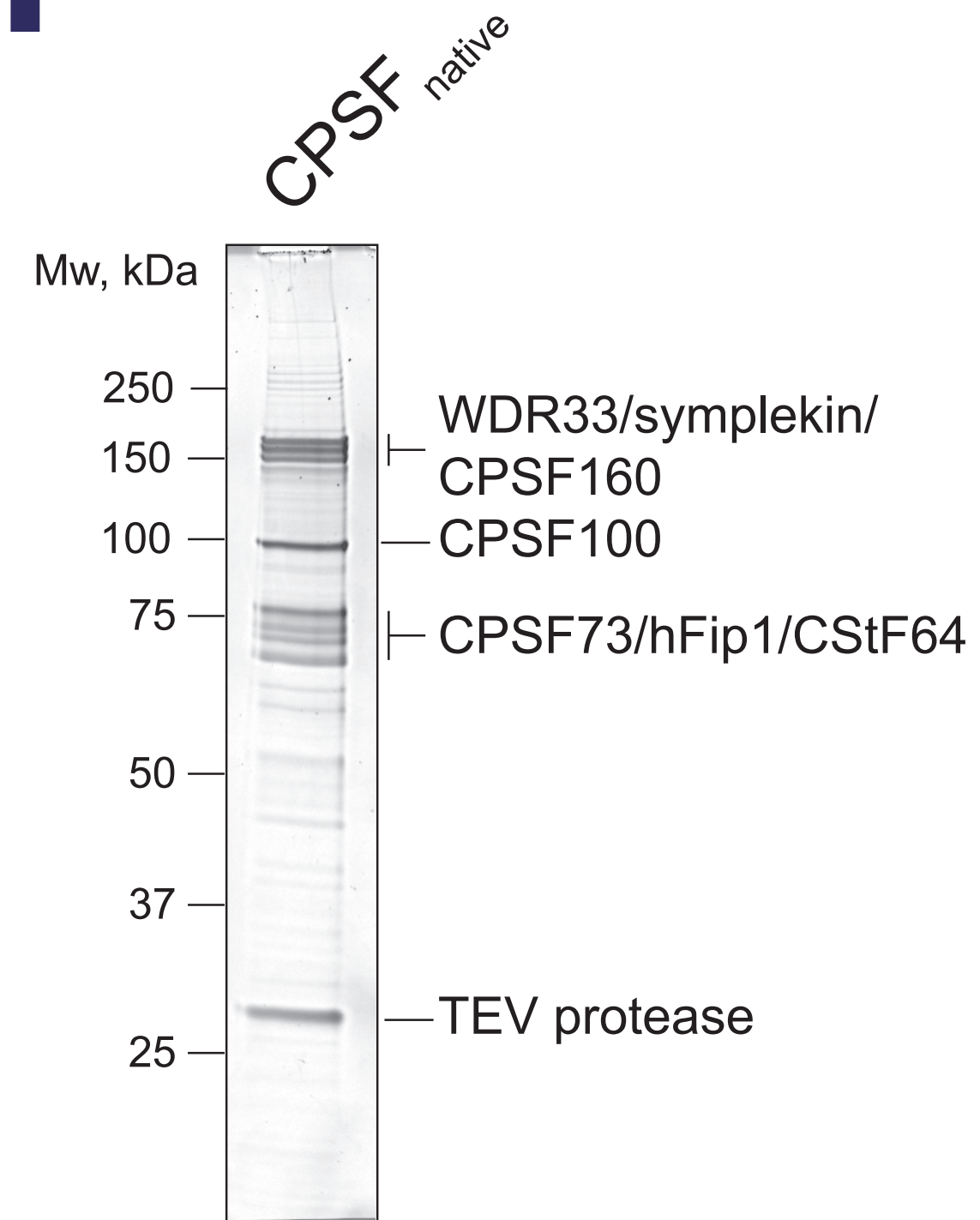
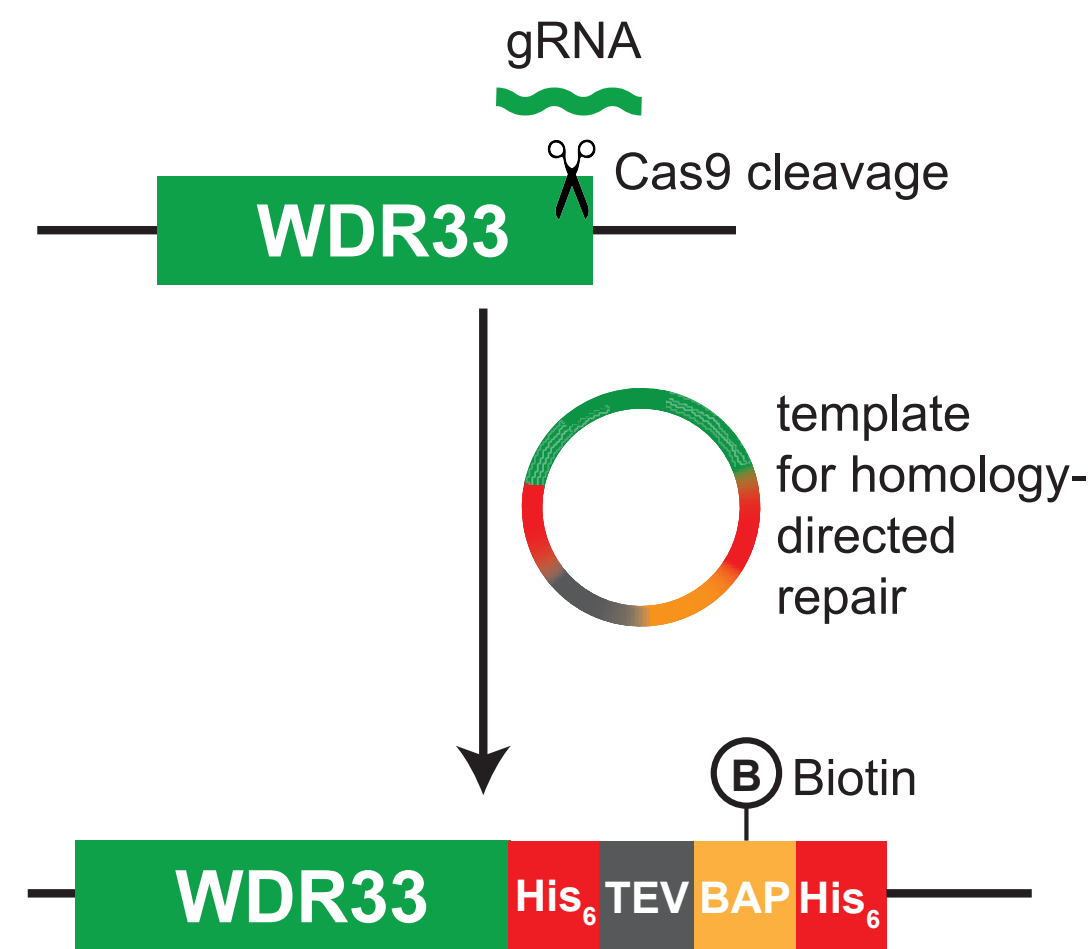
RBBP6/Mpe1 is not a core subunit of human CPSF



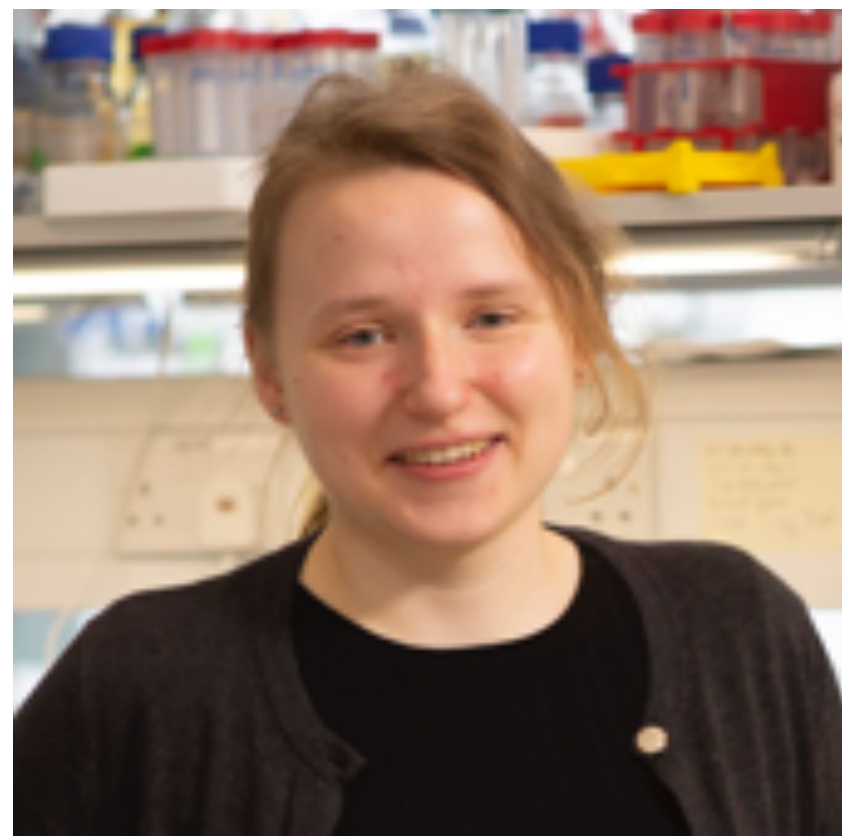
Vytaute Boreikaite



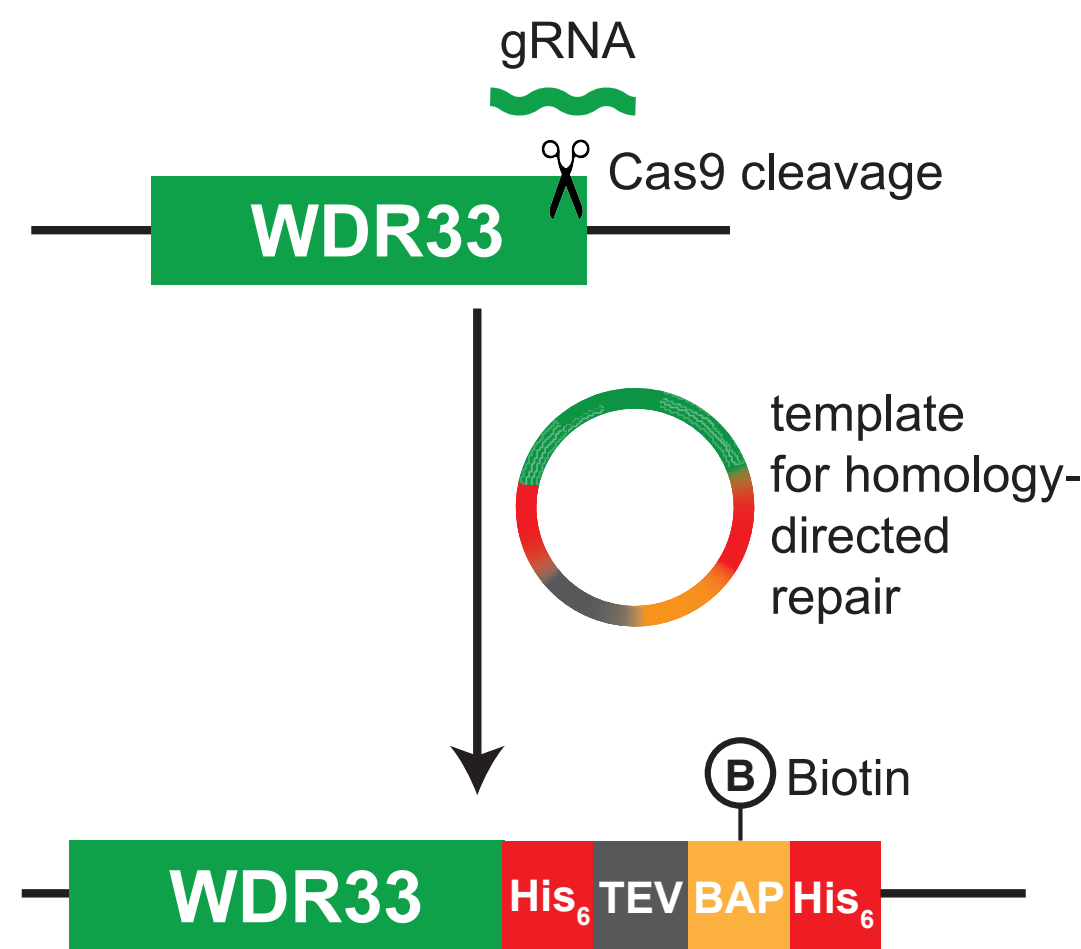
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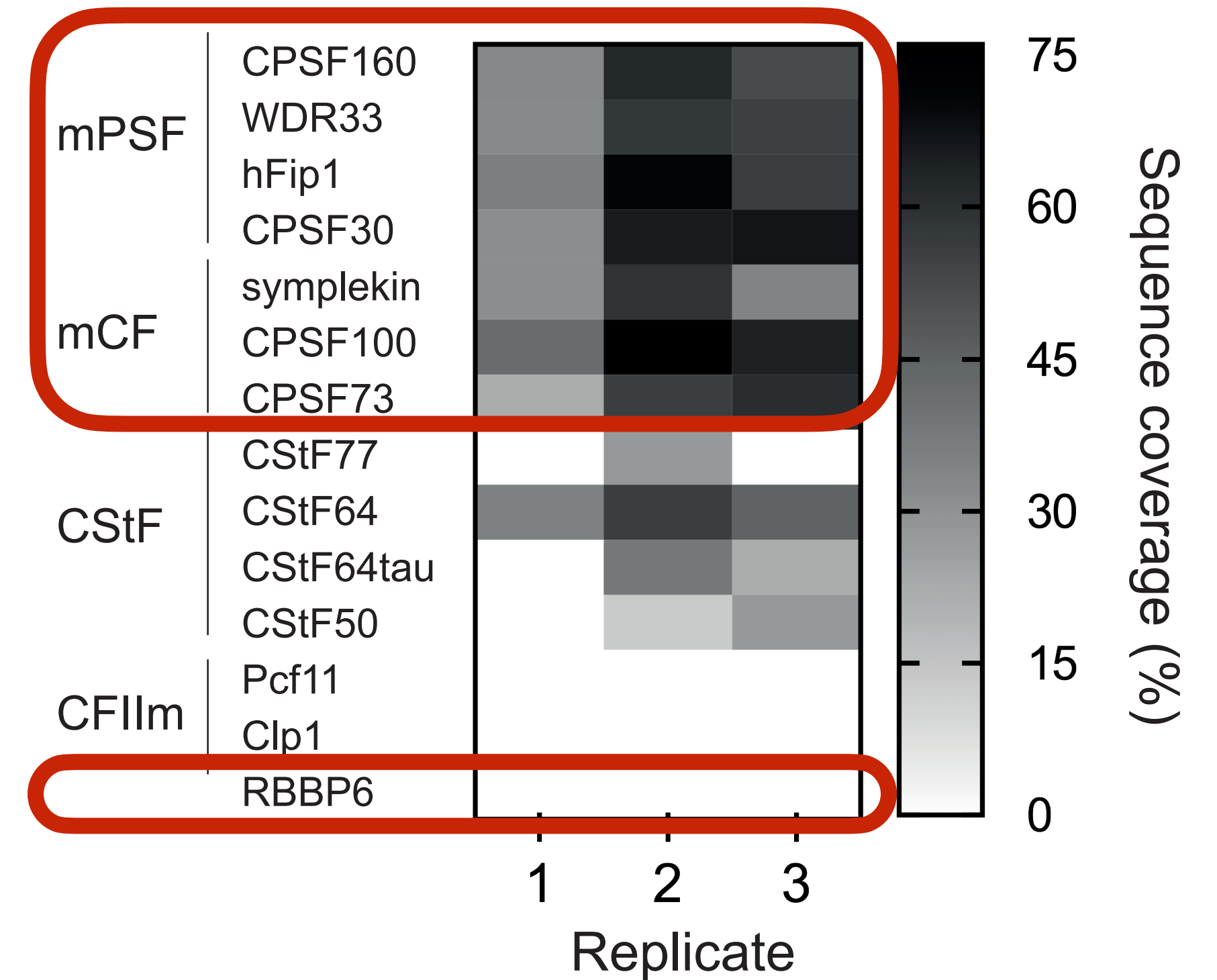
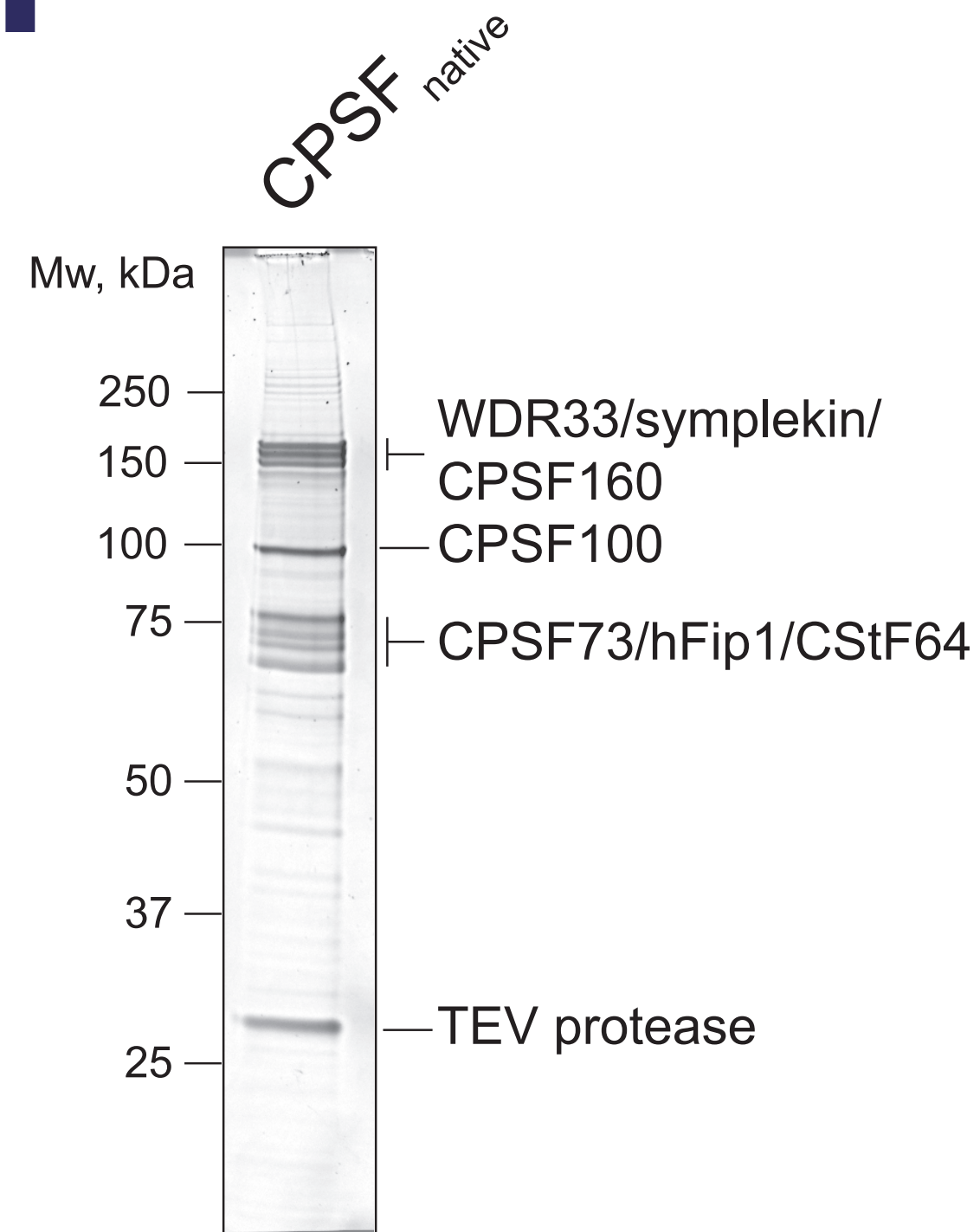
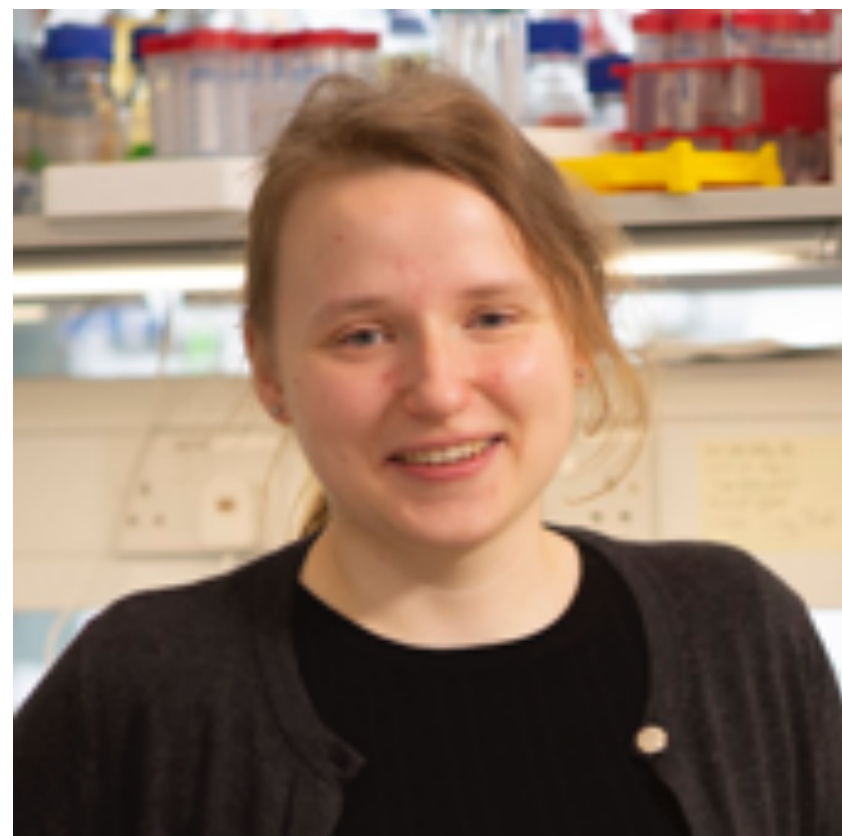
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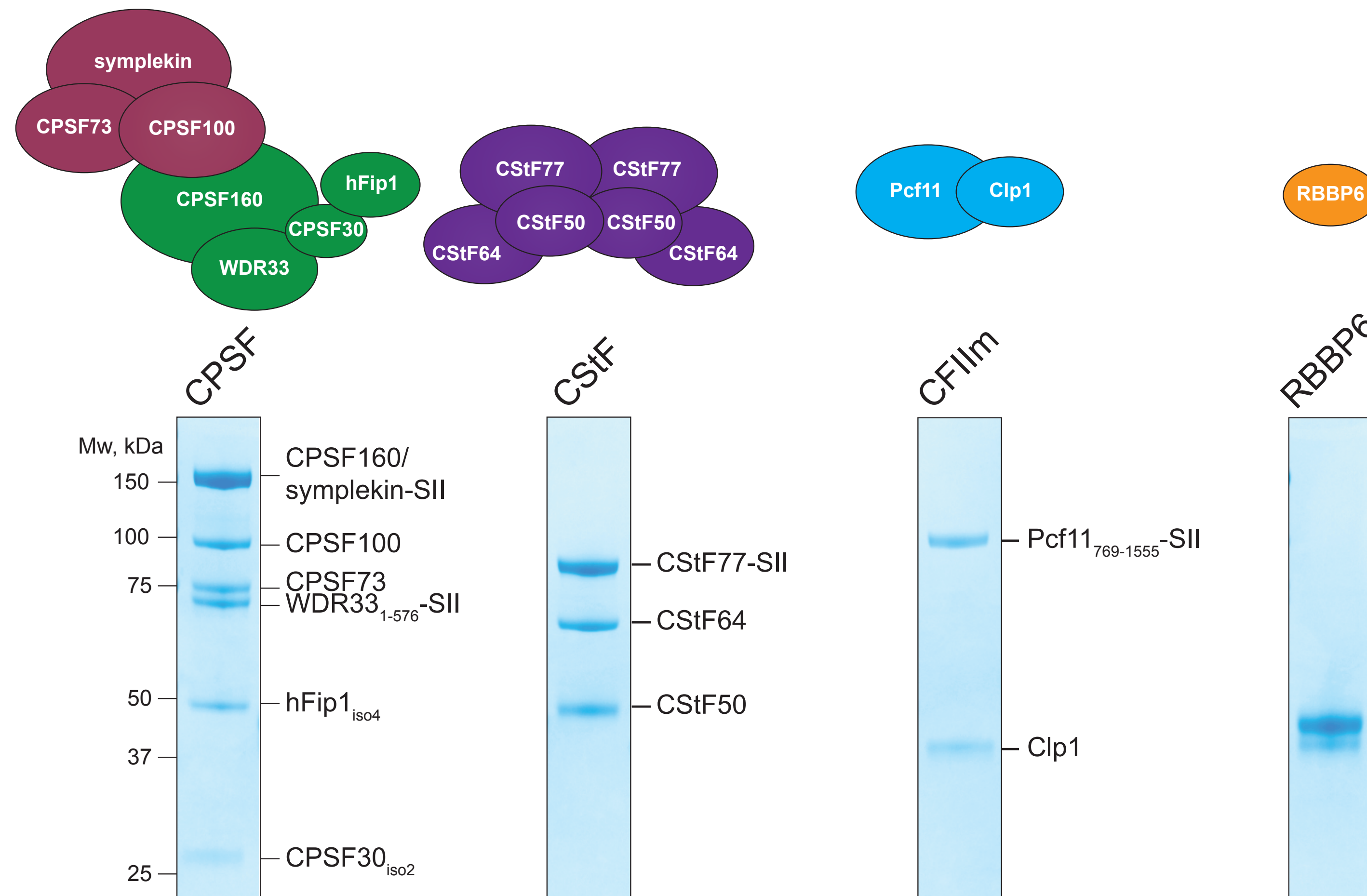
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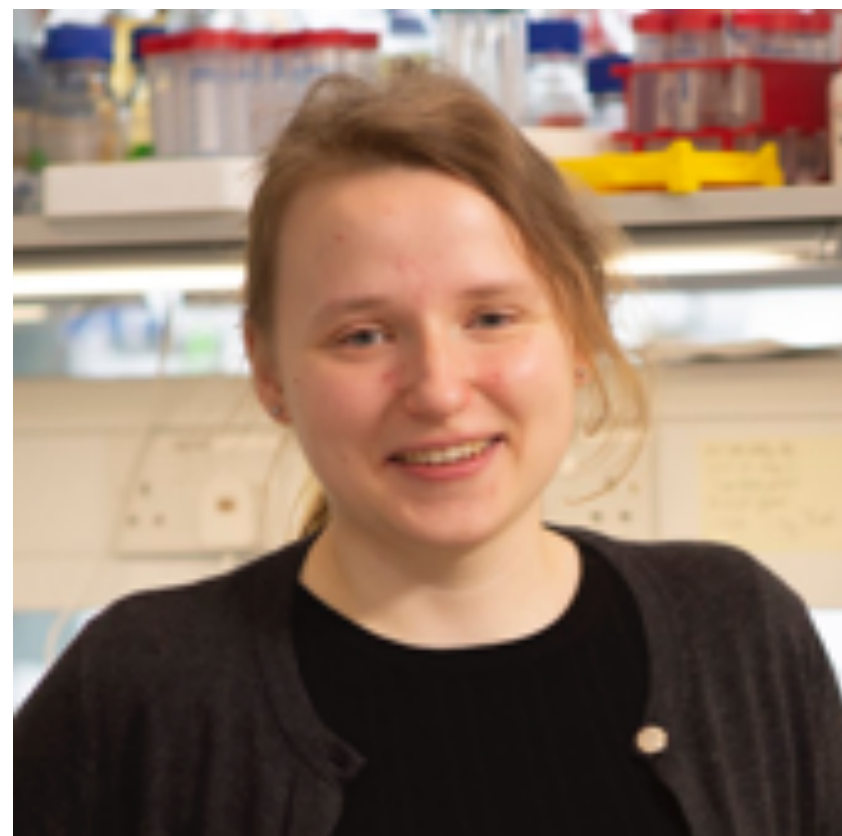
Vytaute Boreikaite



RBBP6 activates human pre-mRNA cleavage

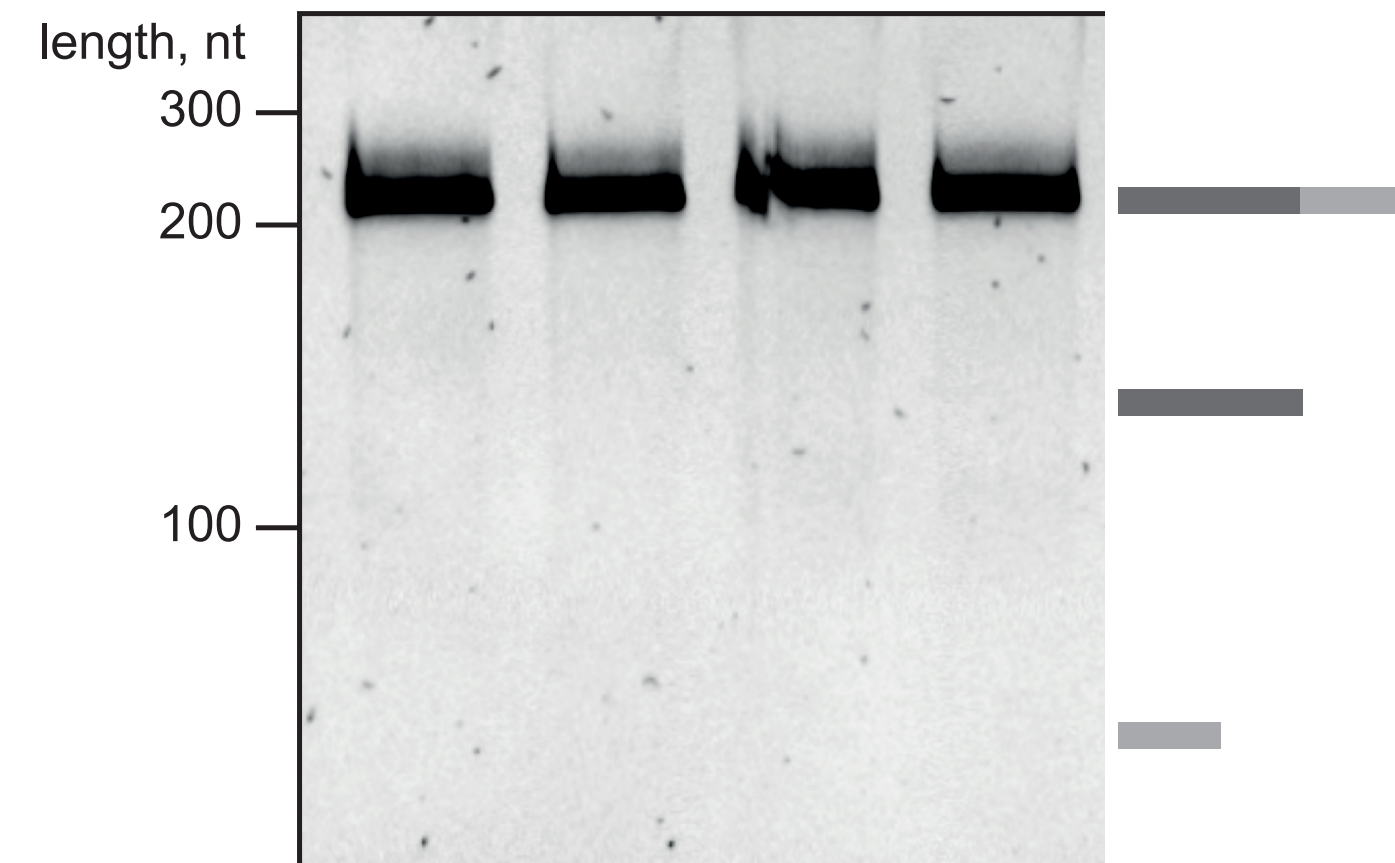


Vytaute Boreikaite



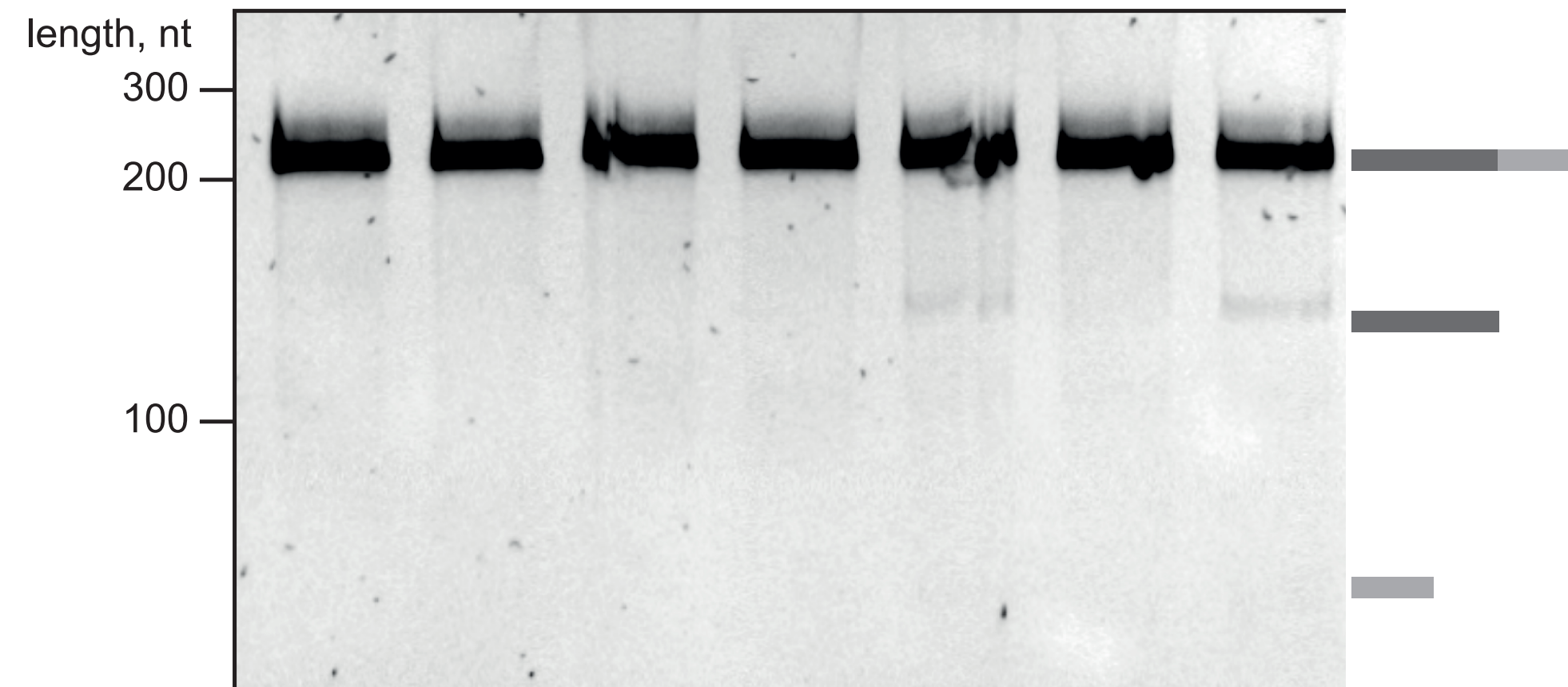
RBBP6 activates human pre-mRNA cleavage

CPSF	+	+	+	+
CStF	-	+	-	+
CFIm	-	-	+	+
RBBP6	-	-	-	-



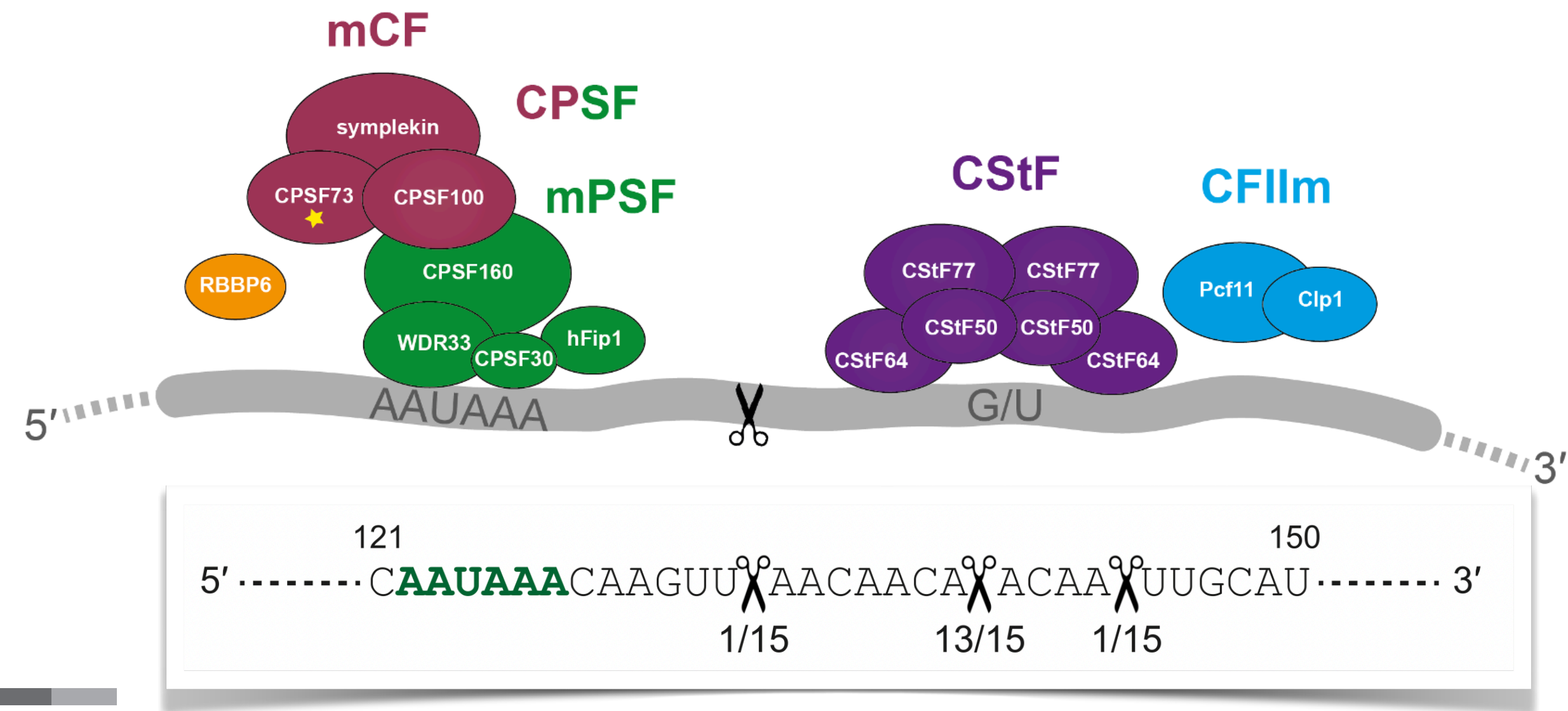
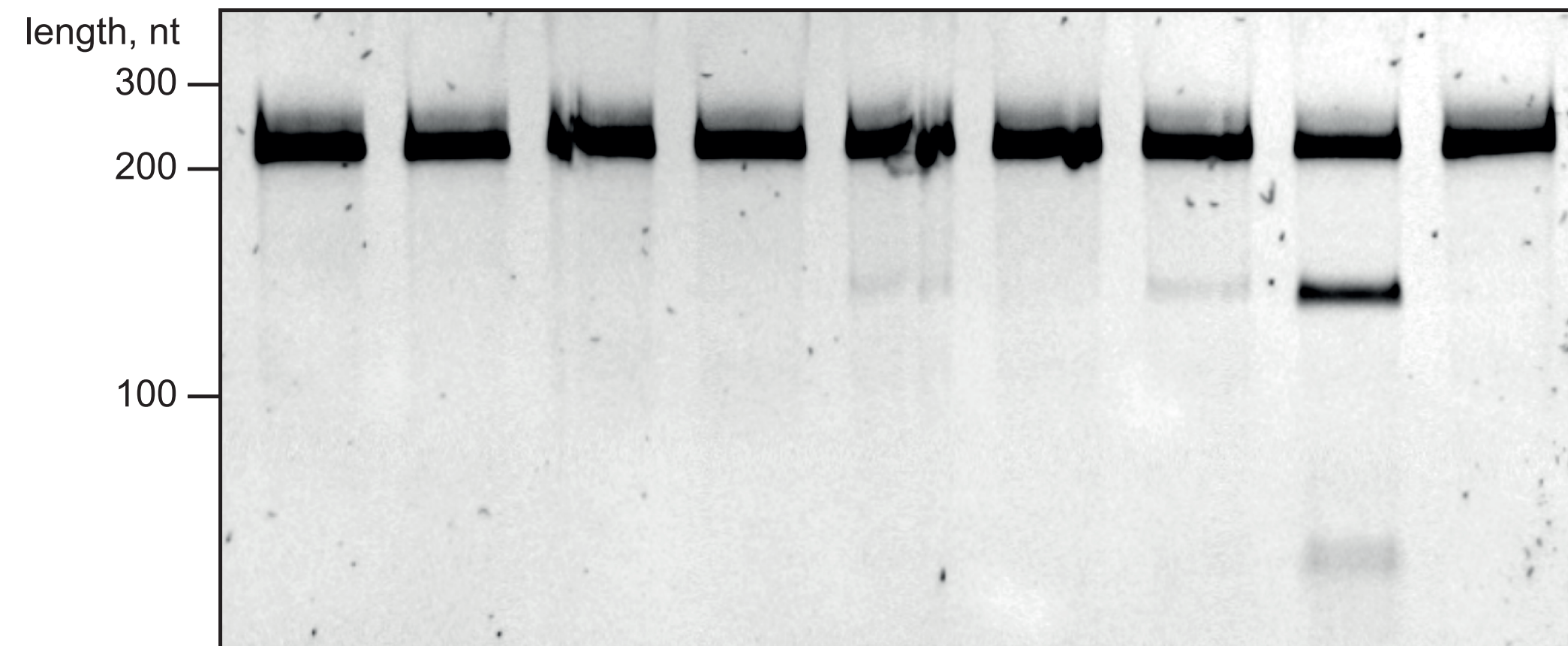
RBBP6 activates human pre-mRNA cleavage

CPSF	+	+	+	+	+	+	+
CStF	-	+	-	+	-	+	-
CFIm	-	-	+	+	-	-	+
RBBP6	-	-	-	-	+	+	+

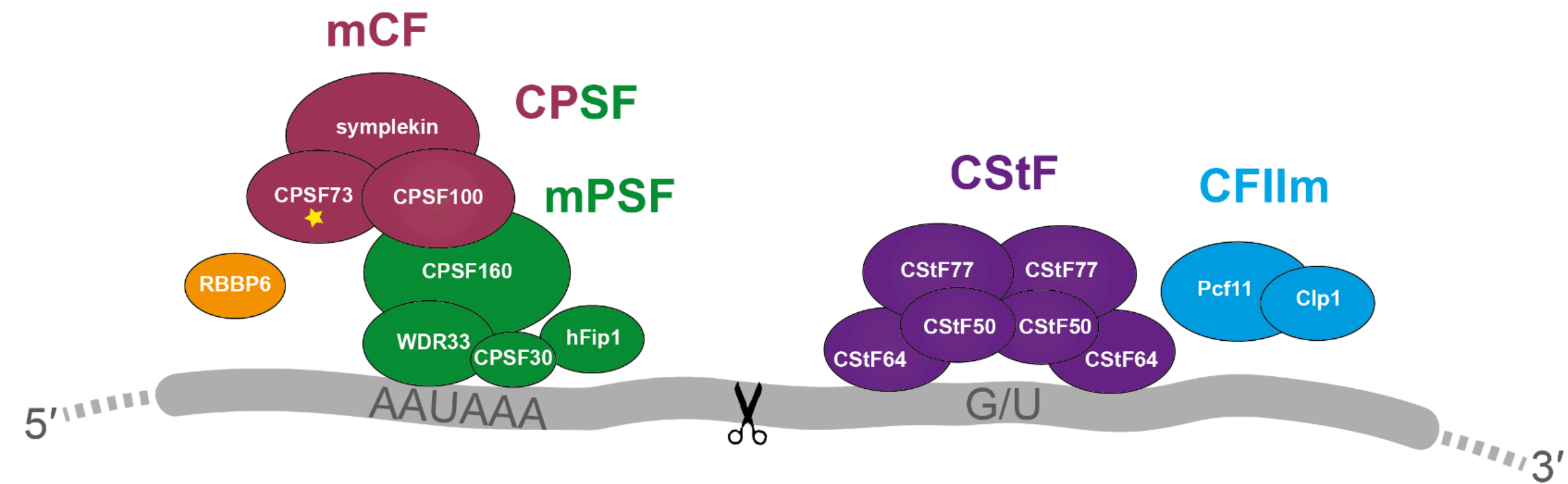
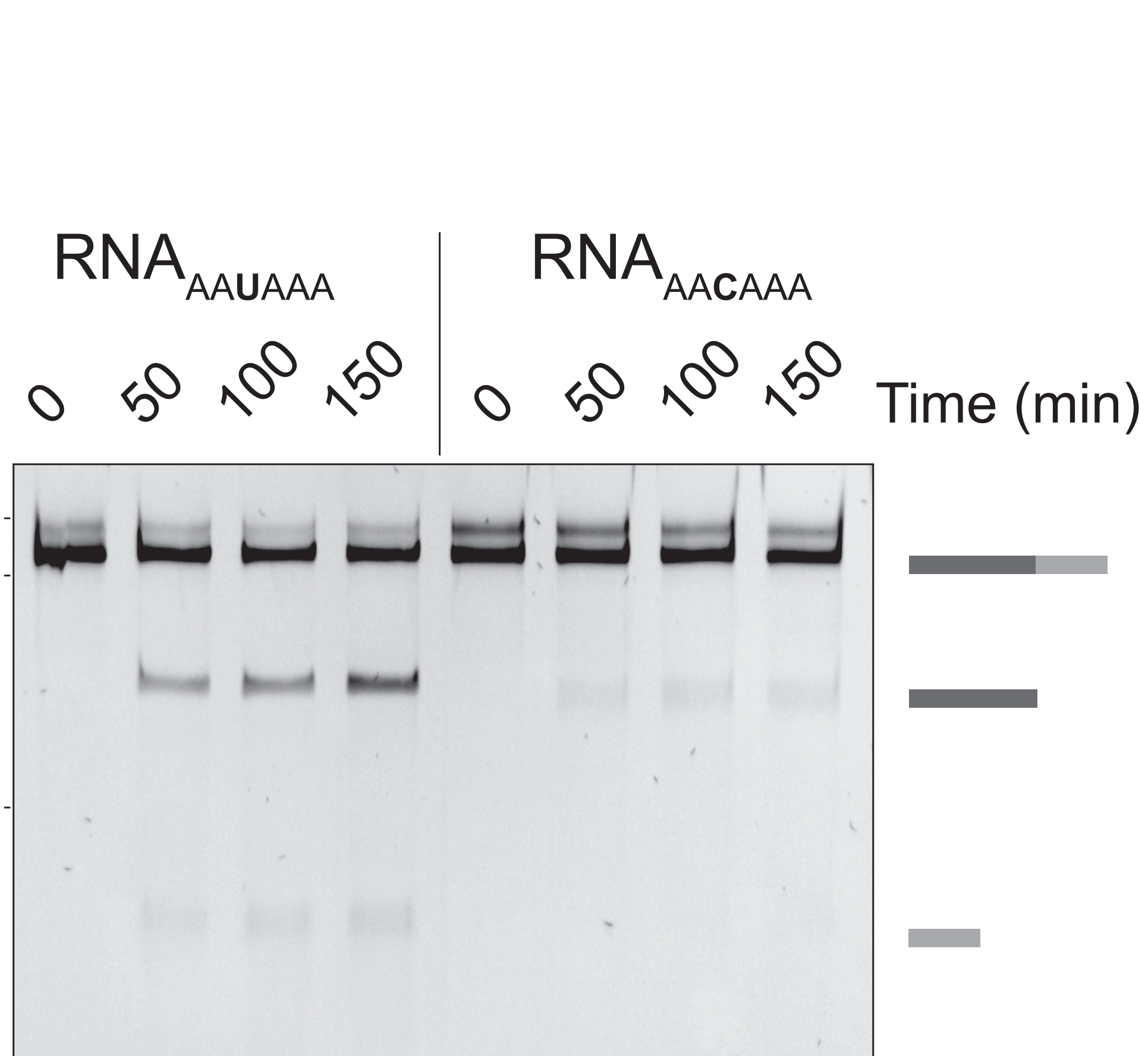


RBBP6 activates human pre-mRNA cleavage

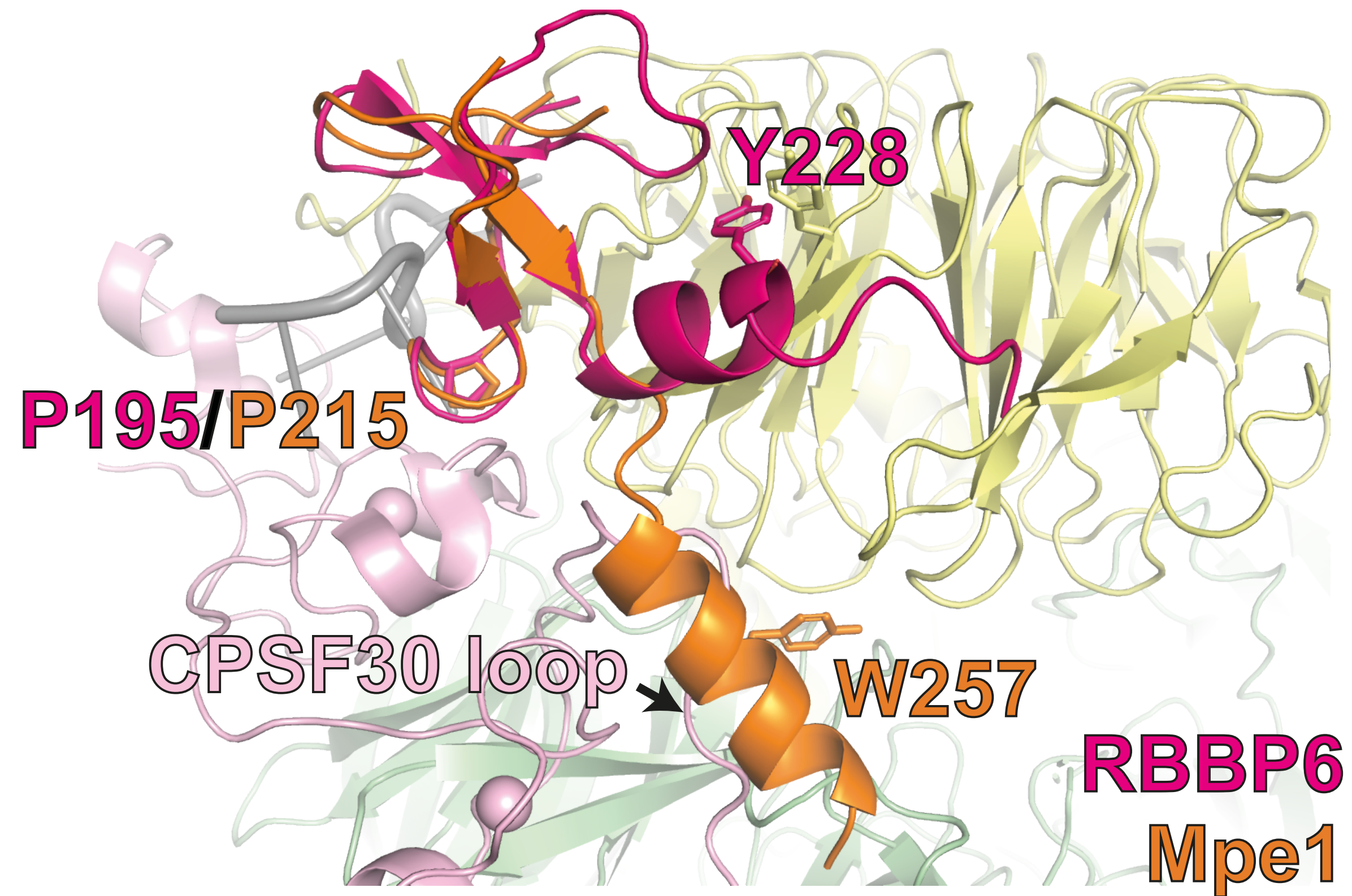
CPSF	+	+	+	+	+	+	+	+	-
CStF	-	+	-	+	-	+	-	+	+
CFIIm	-	-	+	+	-	-	+	+	+
RBBP6	-	-	-	-	+	+	+	+	+



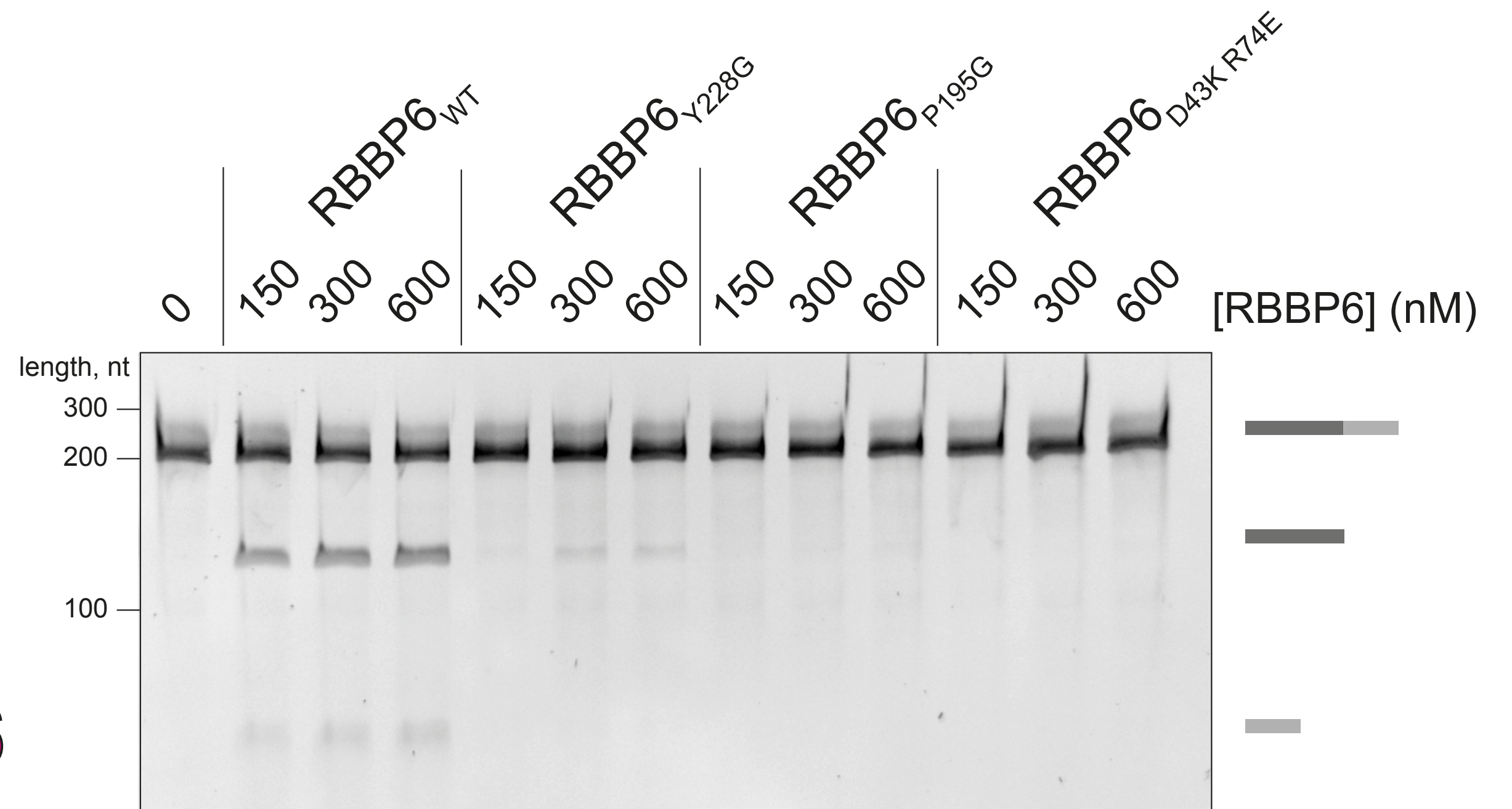
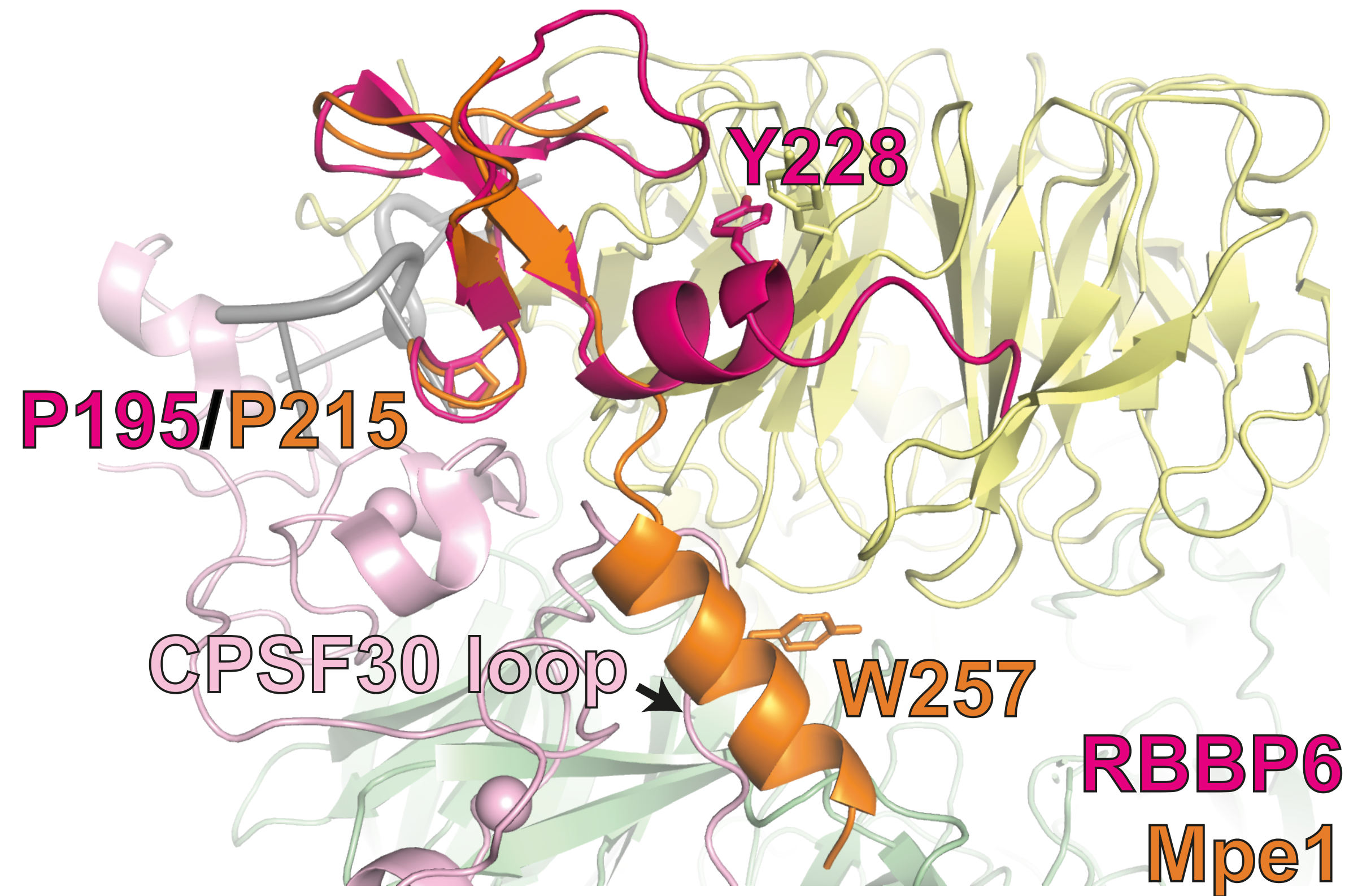
RBBP6 activates human pre-mRNA cleavage



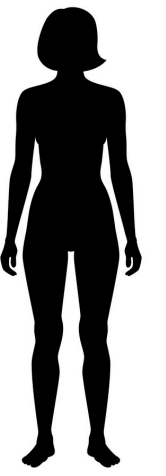
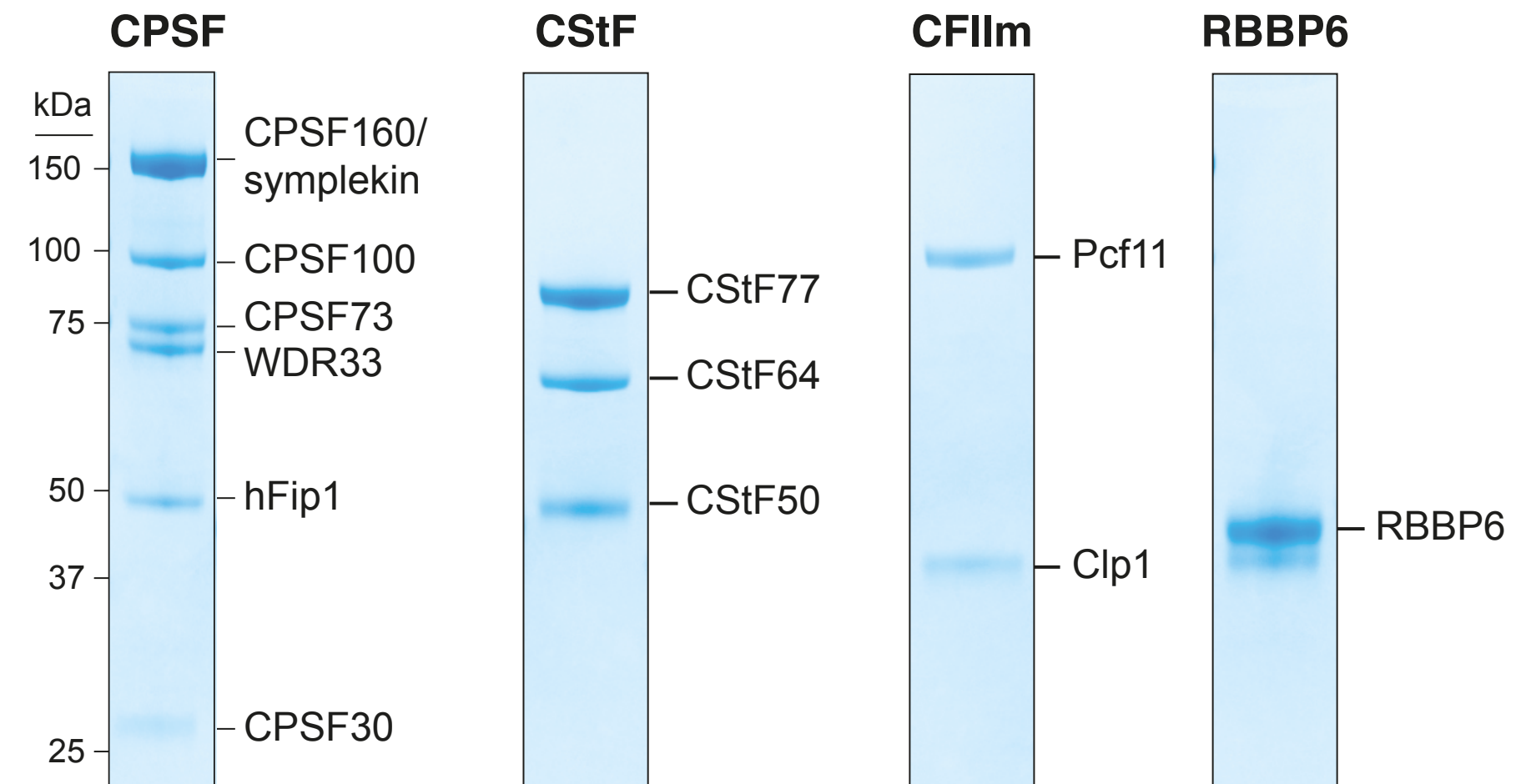
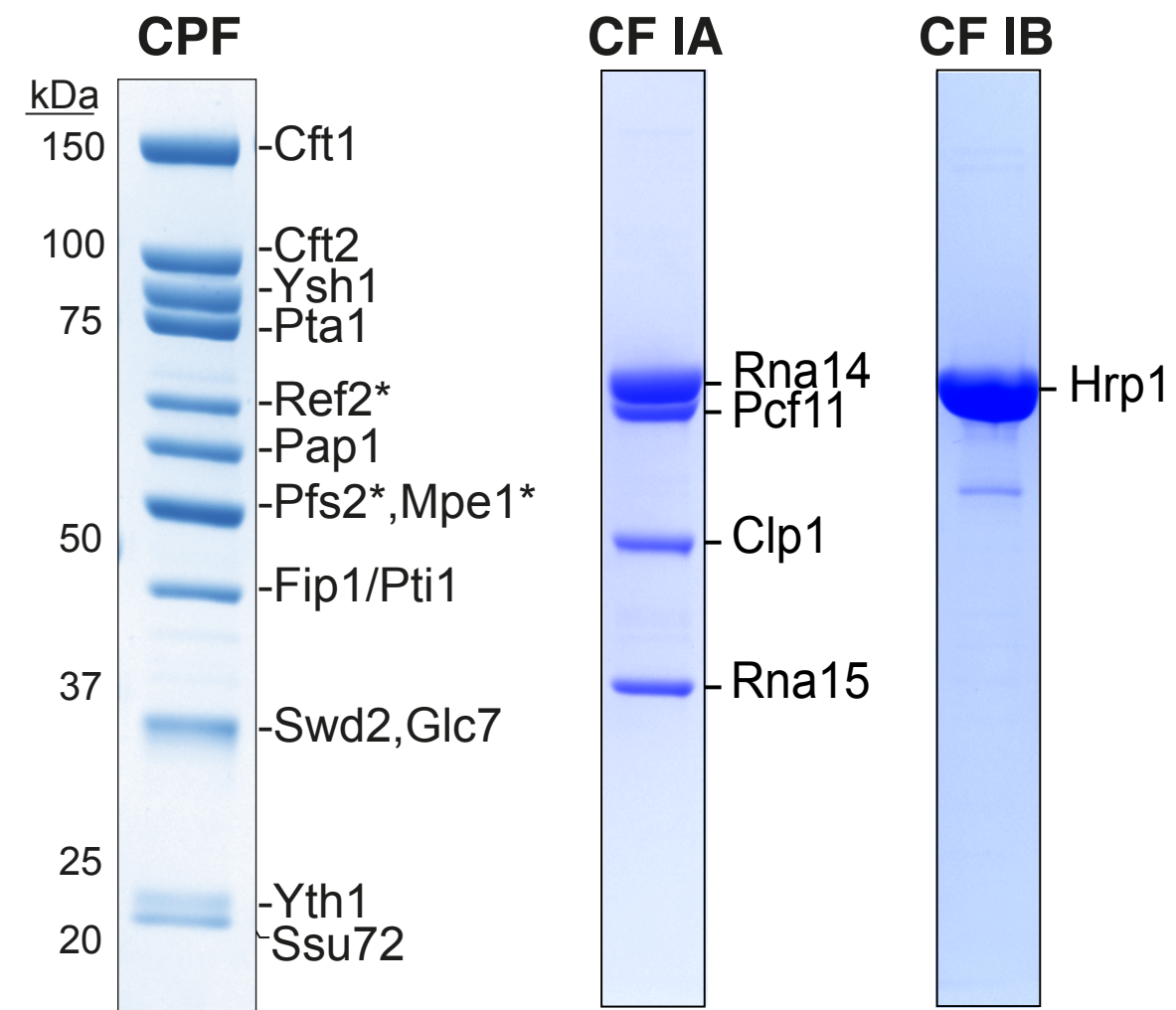
RBBP6 activates human pre-mRNA cleavage



RBBP6 activates human pre-mRNA cleavage

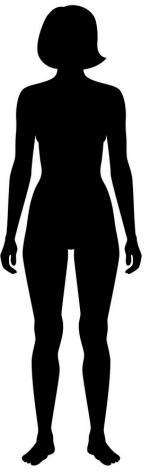
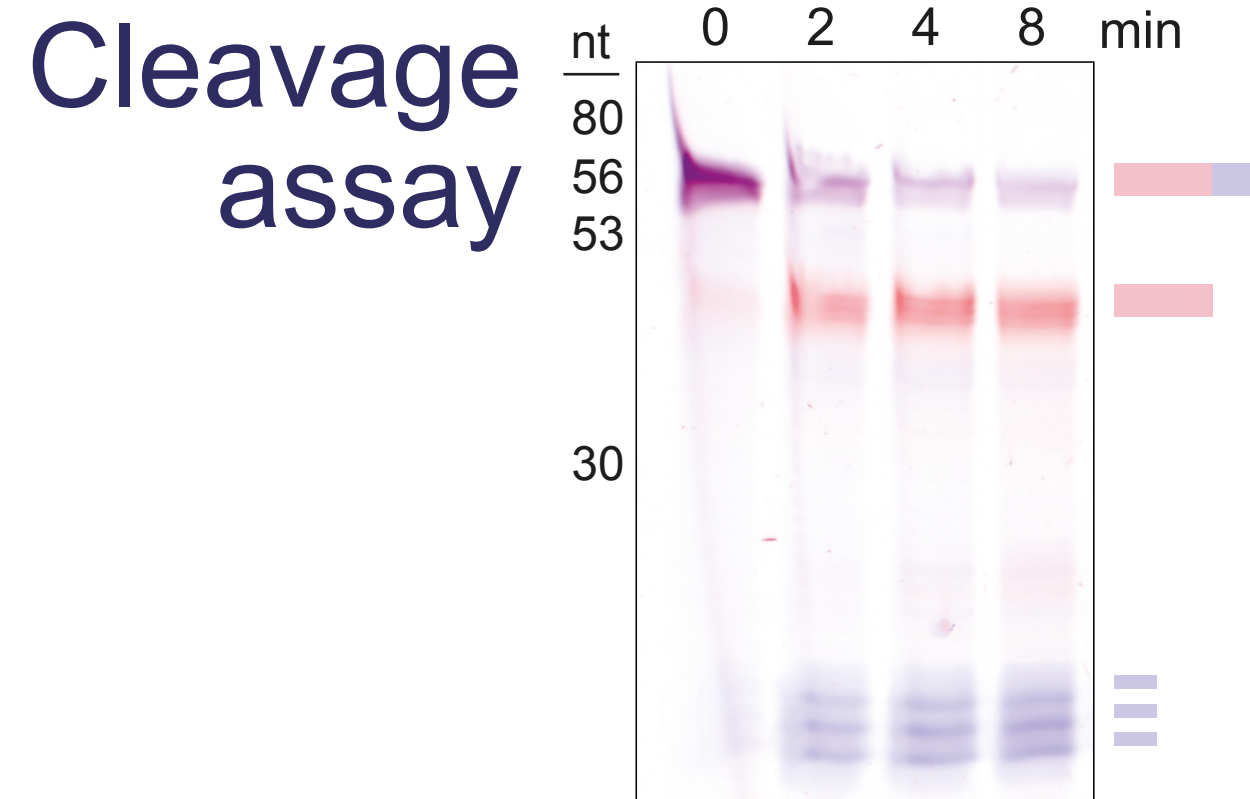
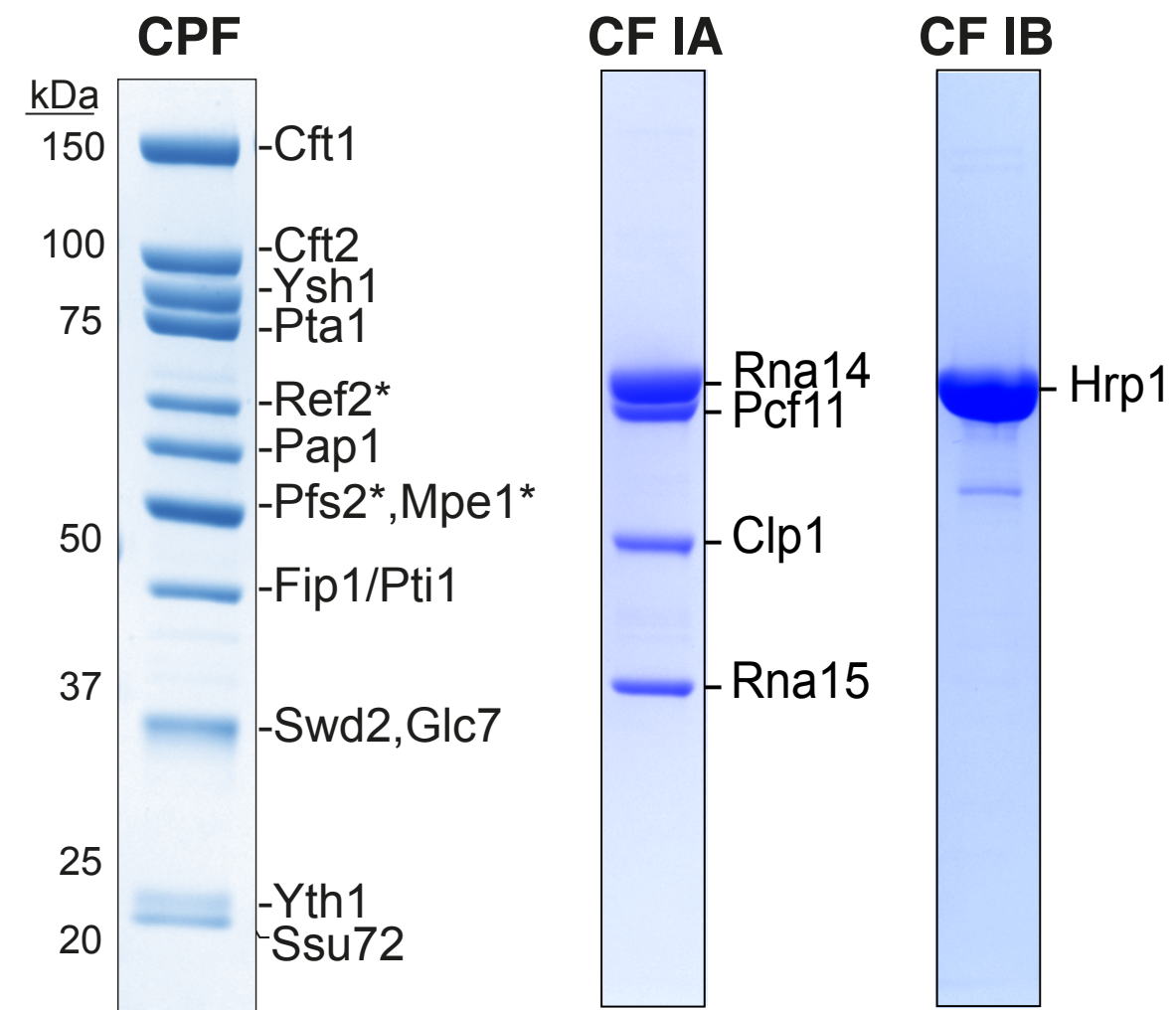


Reconstitution of 3'-end processing

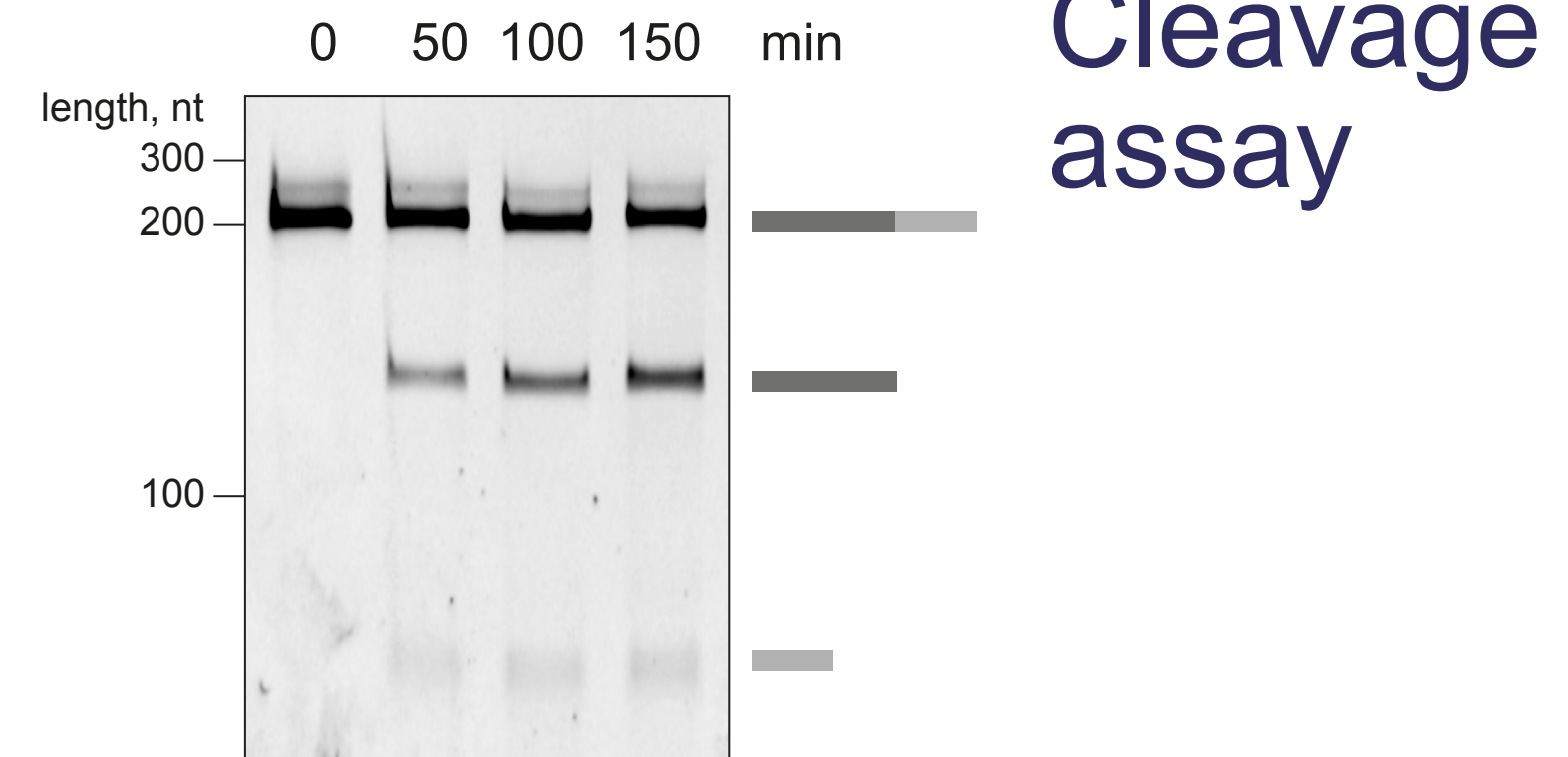
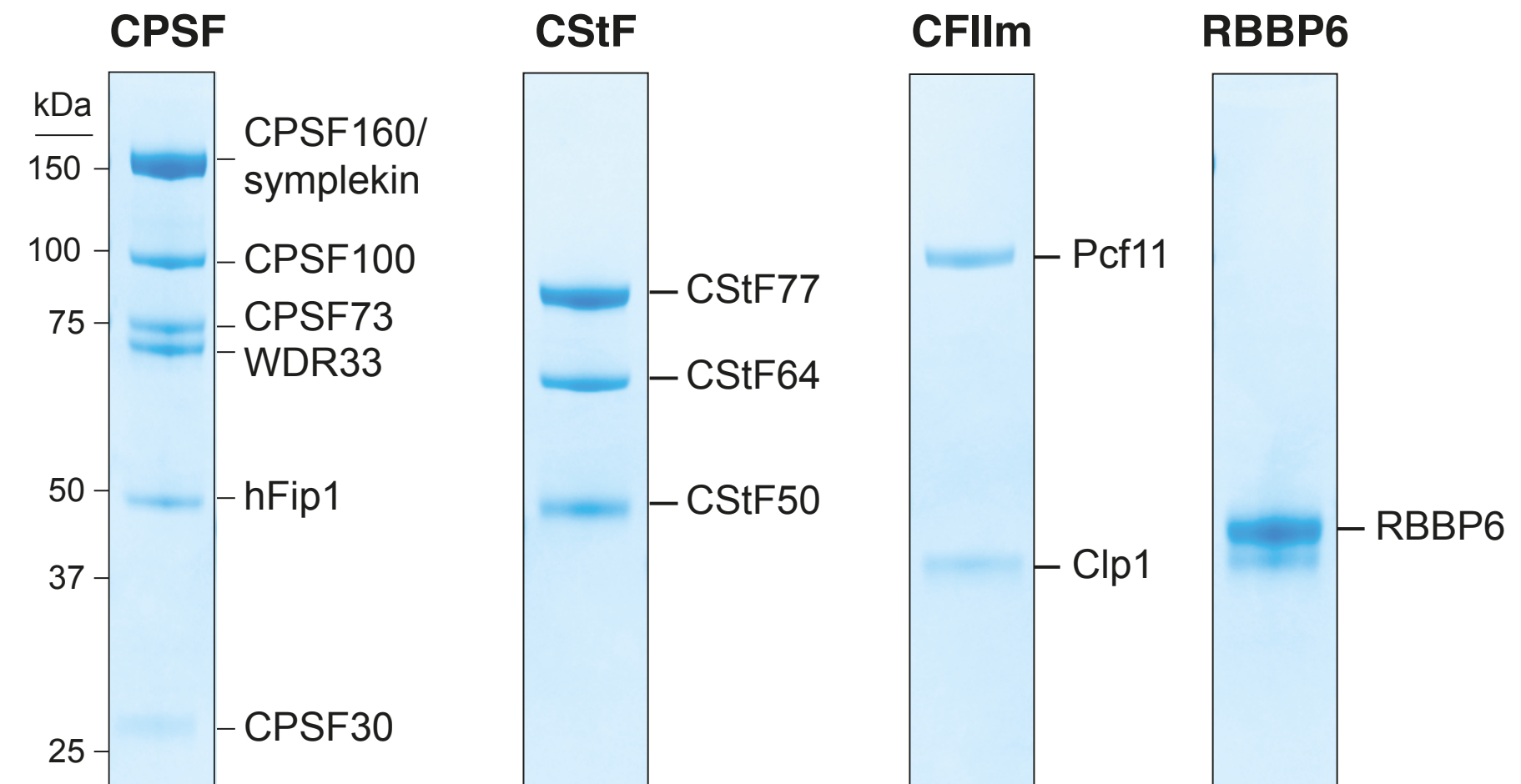


Human

Reconstitution of 3'-end processing



Human



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Native Mass Spectrometry: **Yuliya Gordiyenko**, Carol Robinson

HDX-MS: Sarah Maslen, Mark Skehel

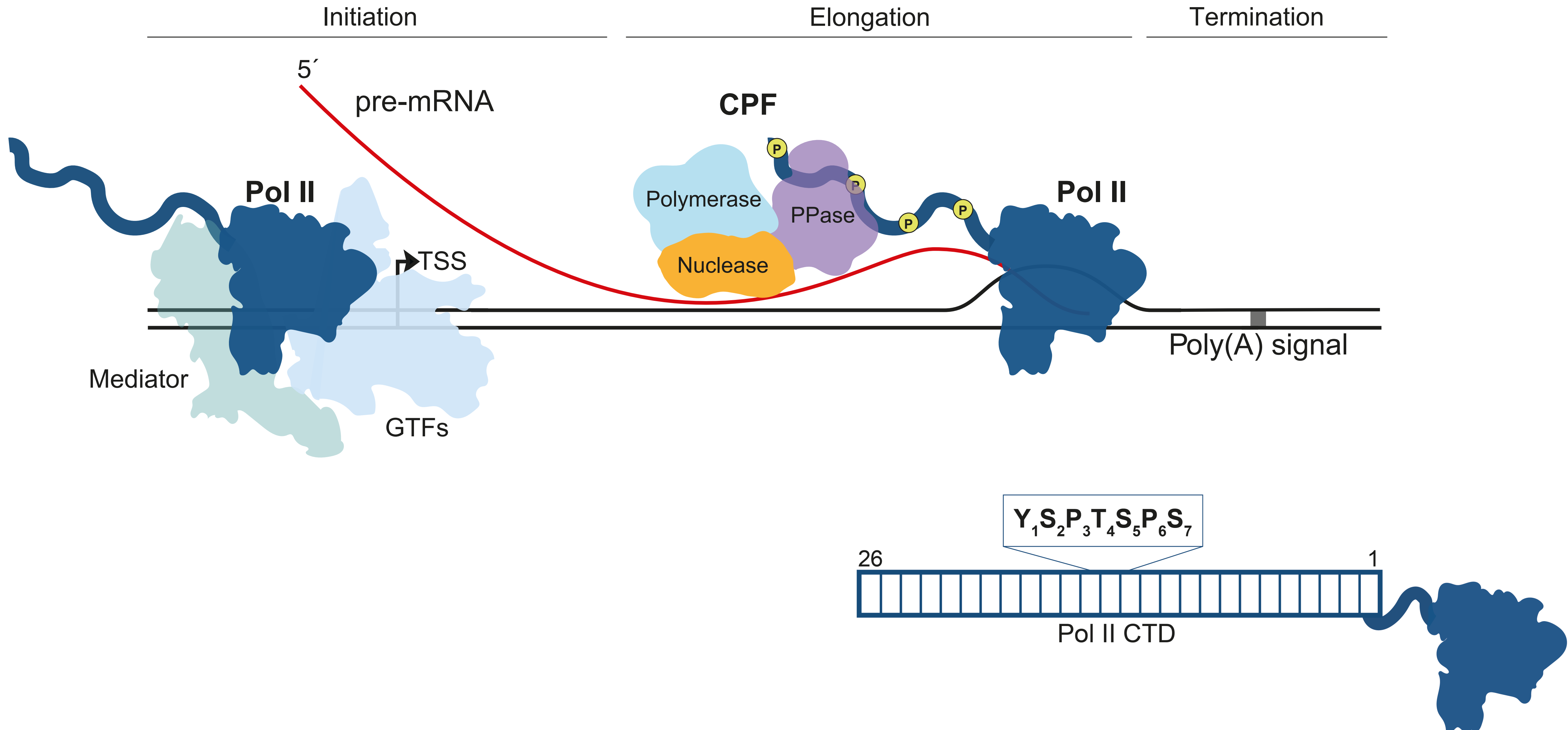
XL-MS: **Francis O'Reilly**, Juri Rappsilber

EM: Christos Savva, Shaoxia Chen, Giuseppe Cannone, Grigory Sharov

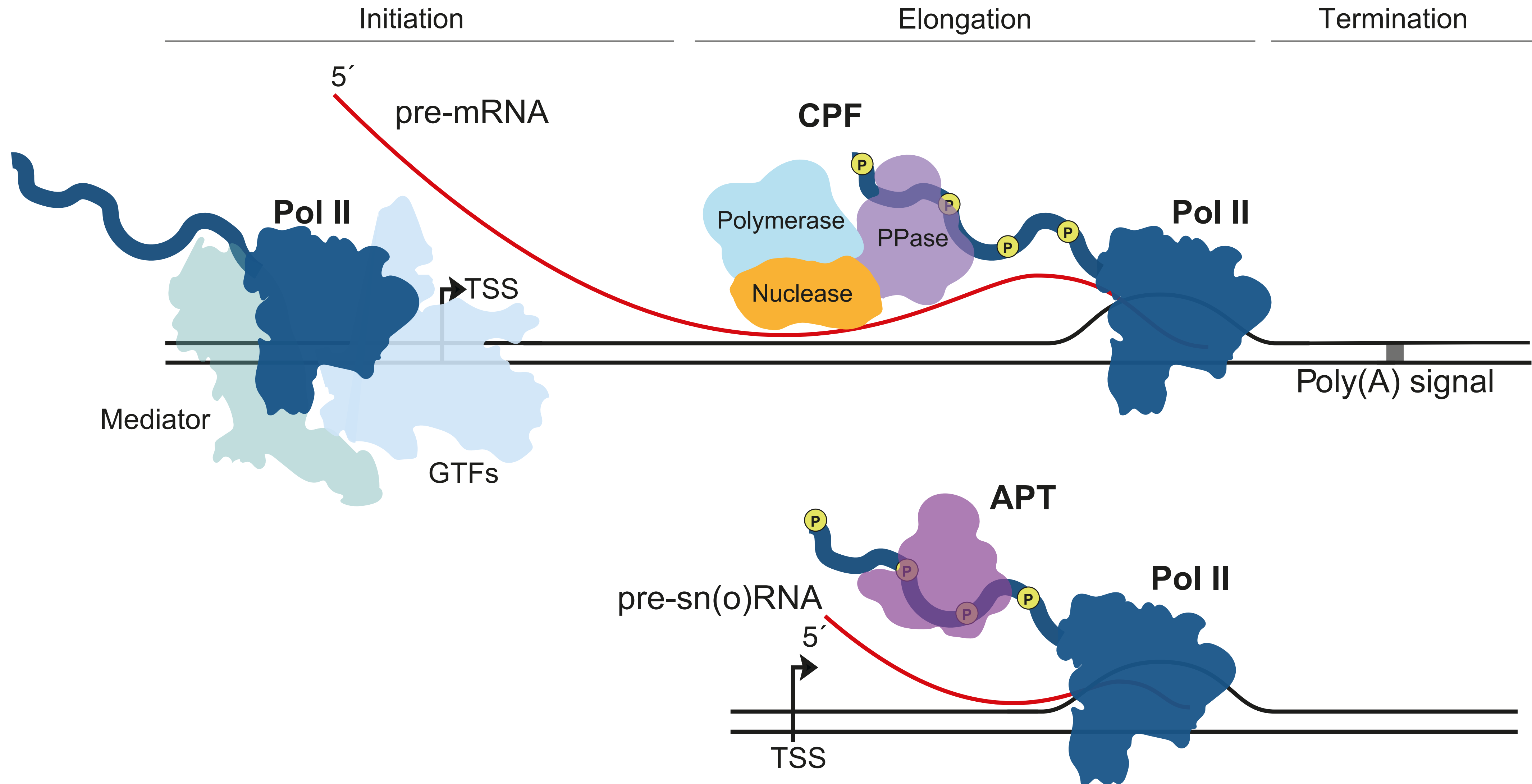
eBIC: Alistair Siebert, Dan Clare, Corey Hecksel



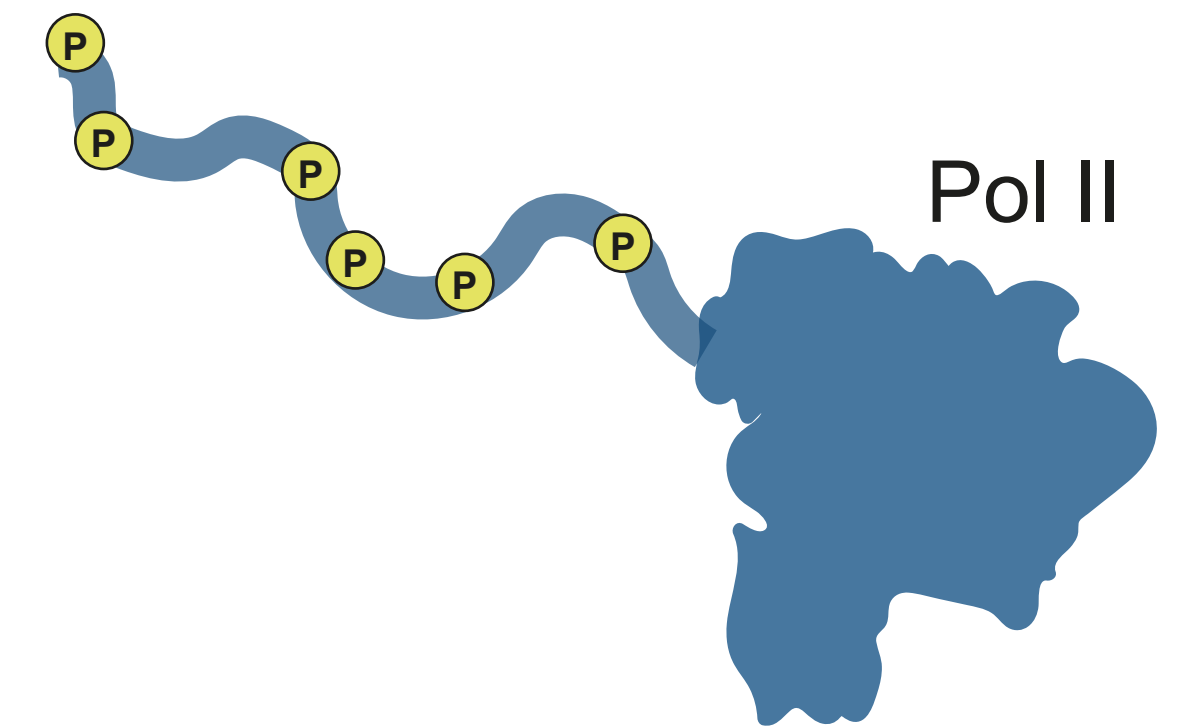
How does CPF interact with Pol II?



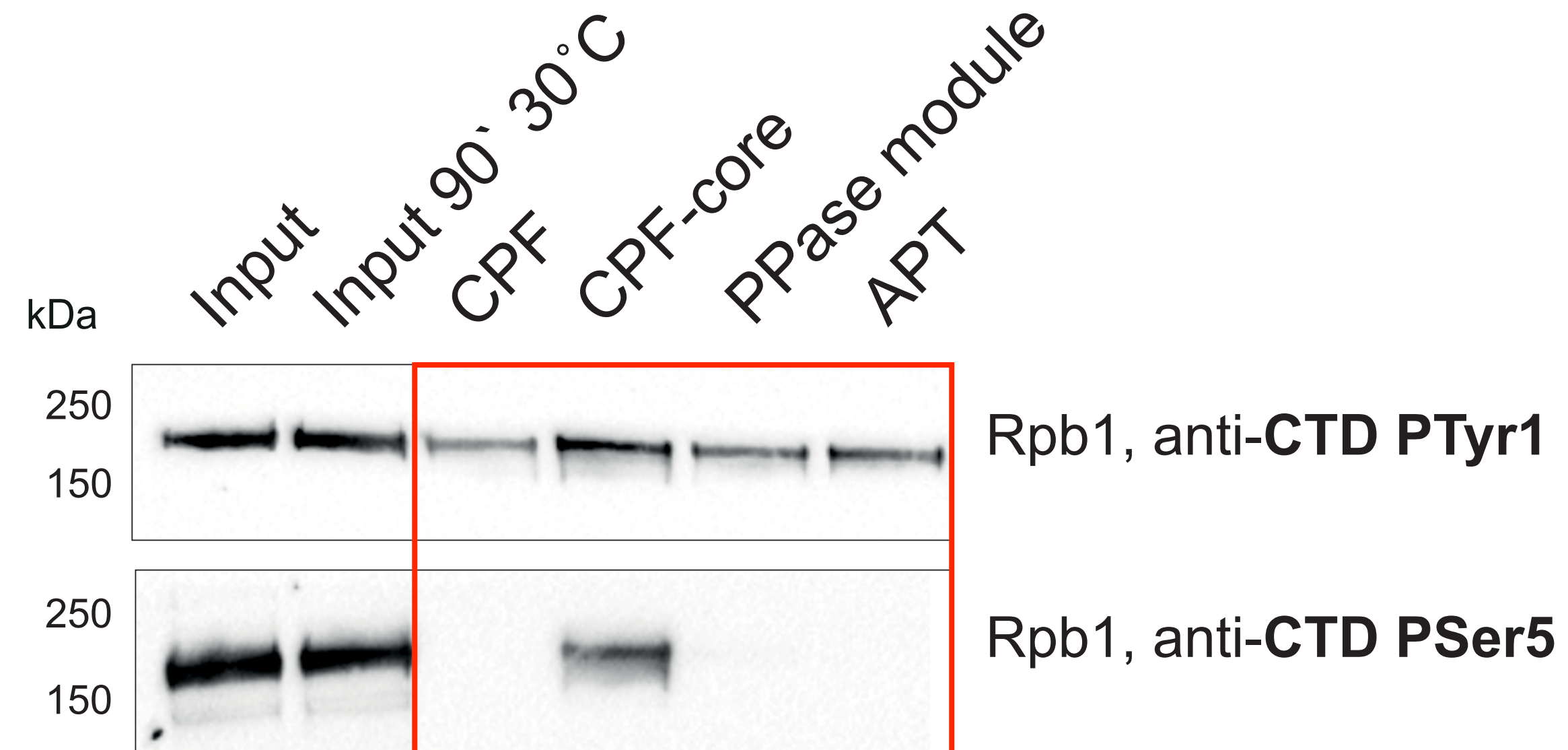
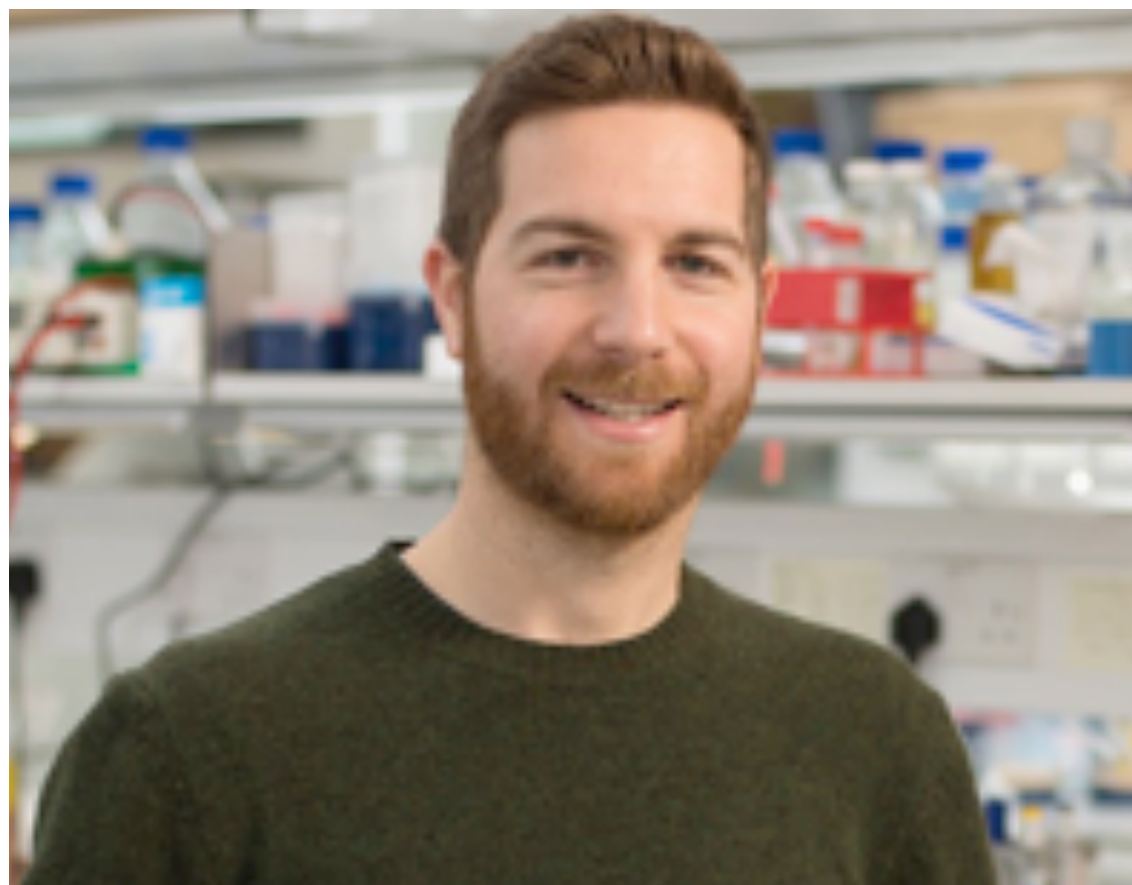
Pol II CTD phosphorylation



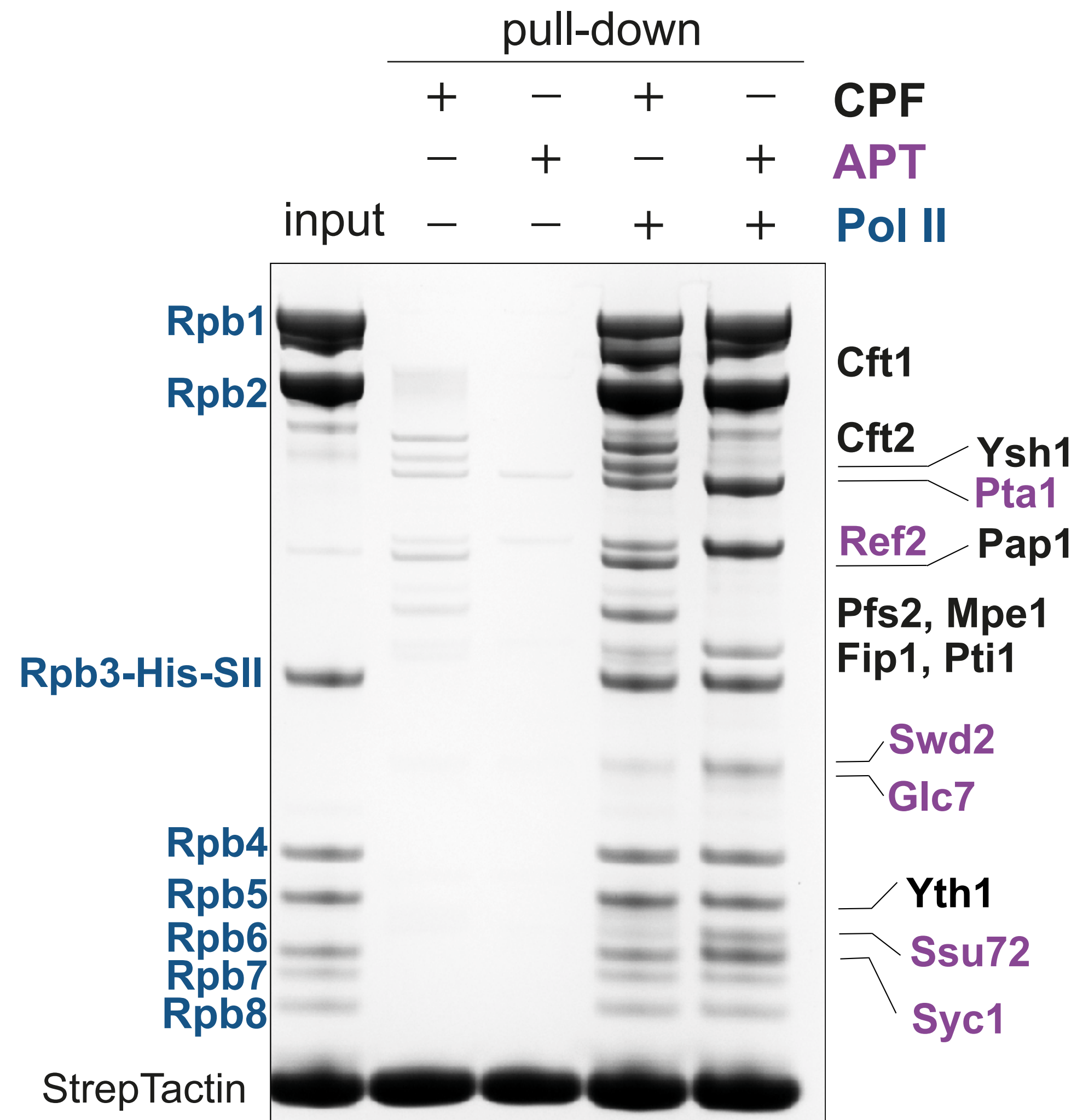
CPF and APT dephosphorylate Pol II CTD



Manuel Carminati

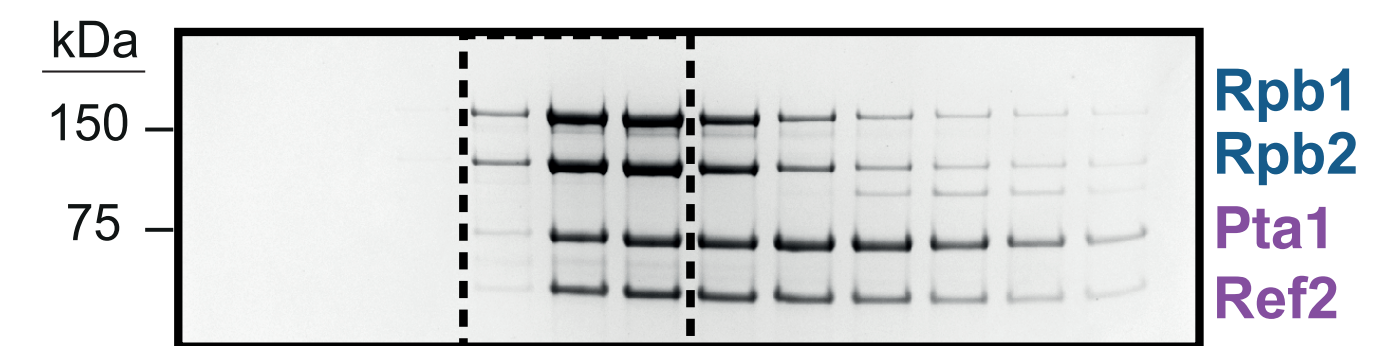
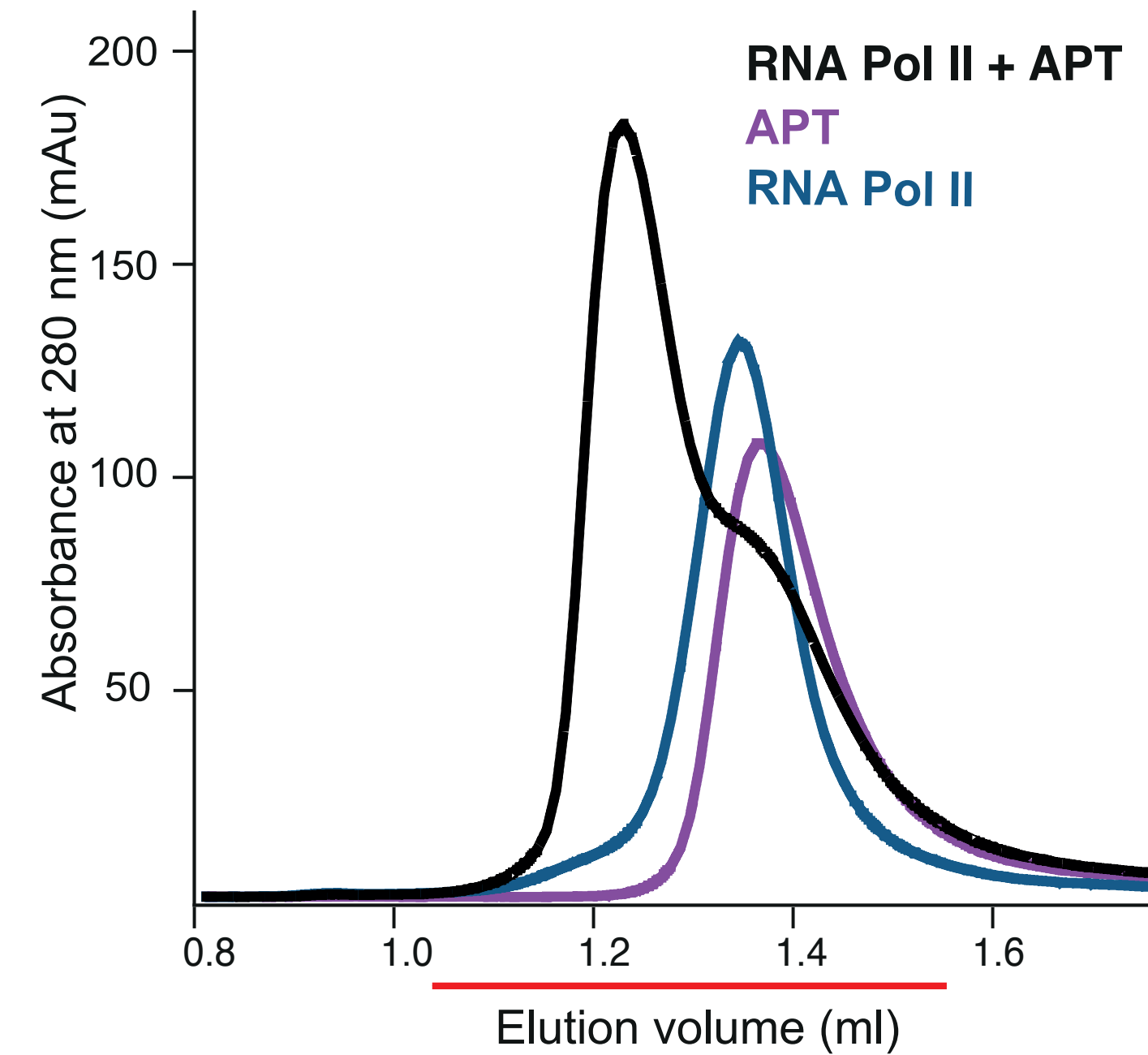
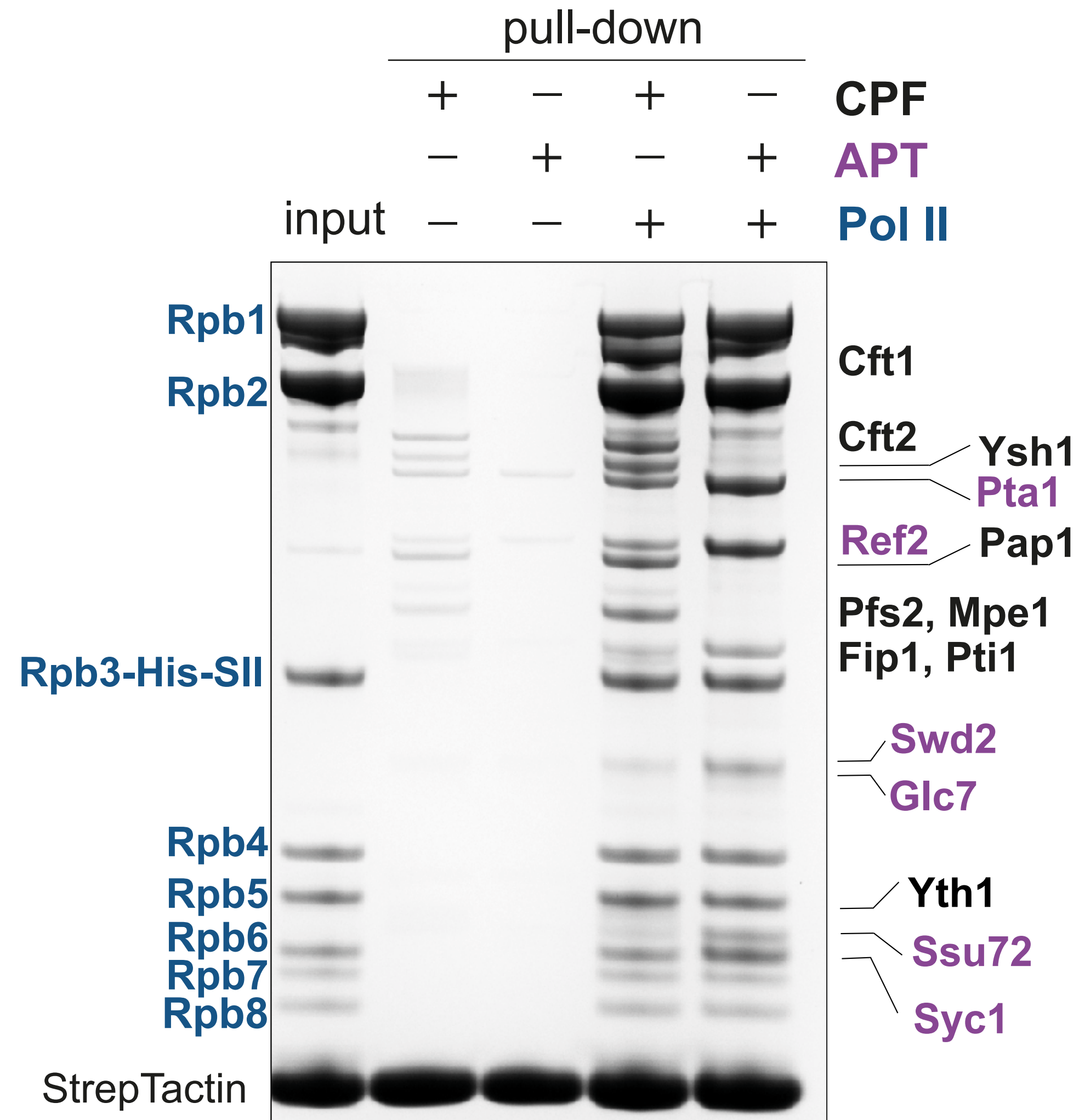


CPF and APT interact directly with Pol II

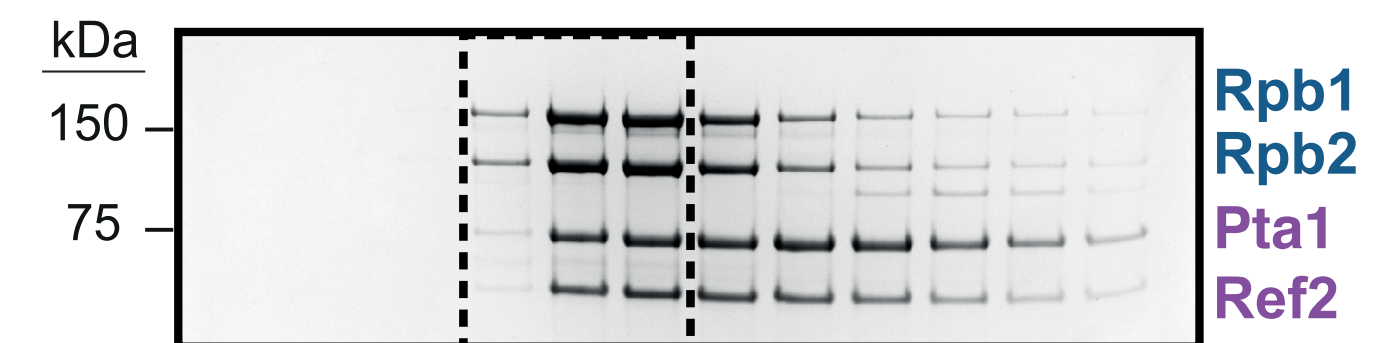
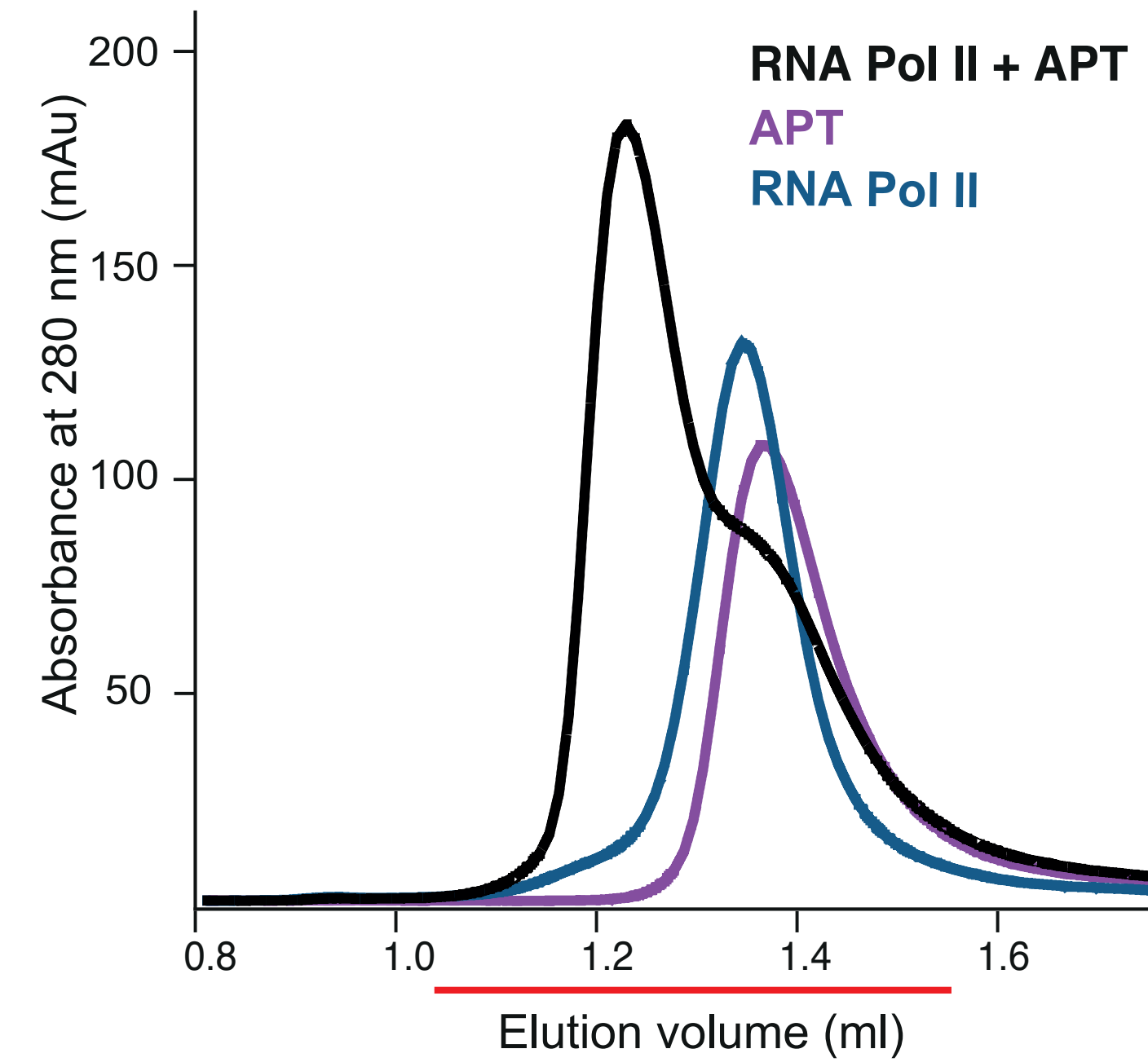
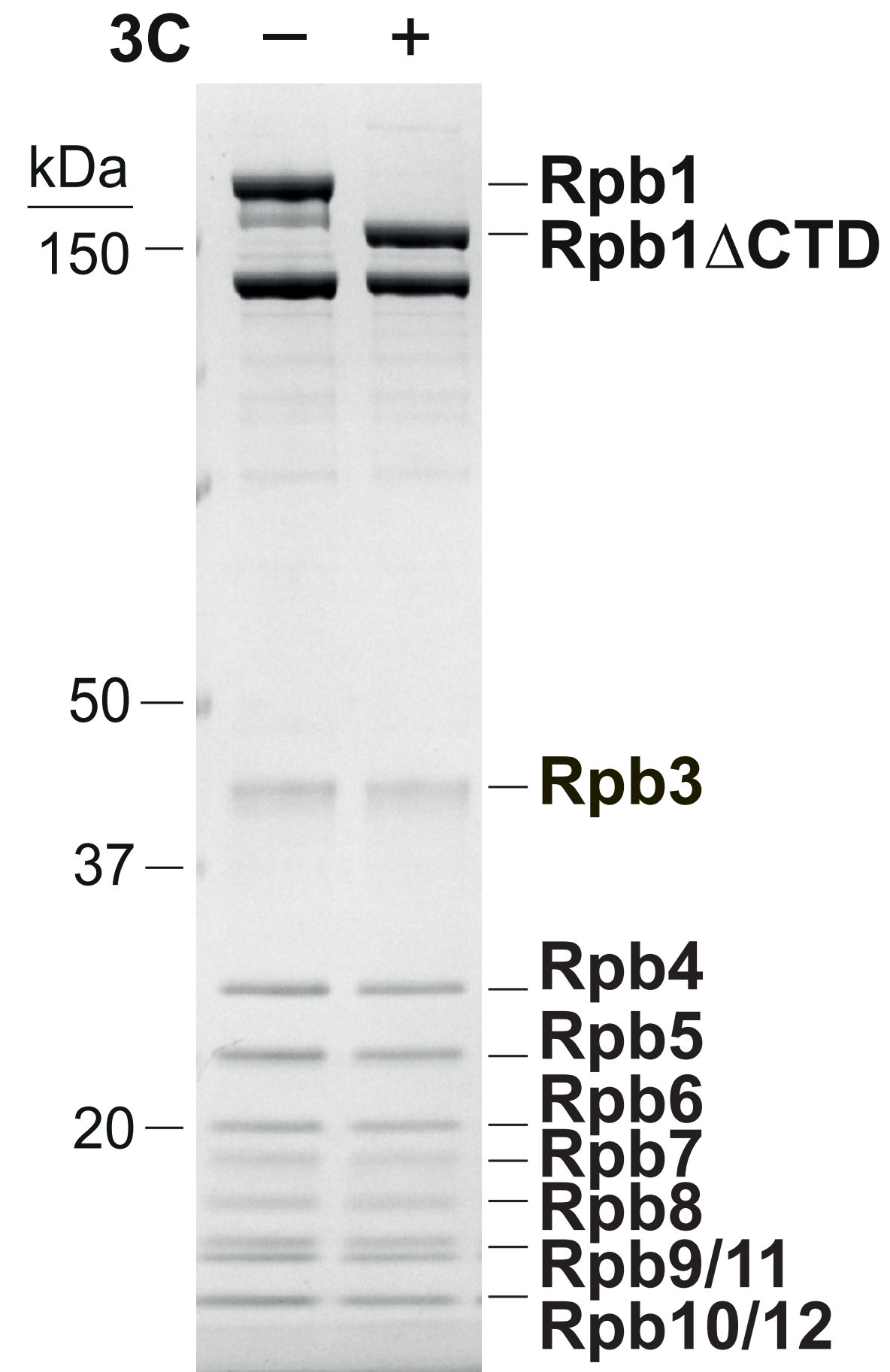
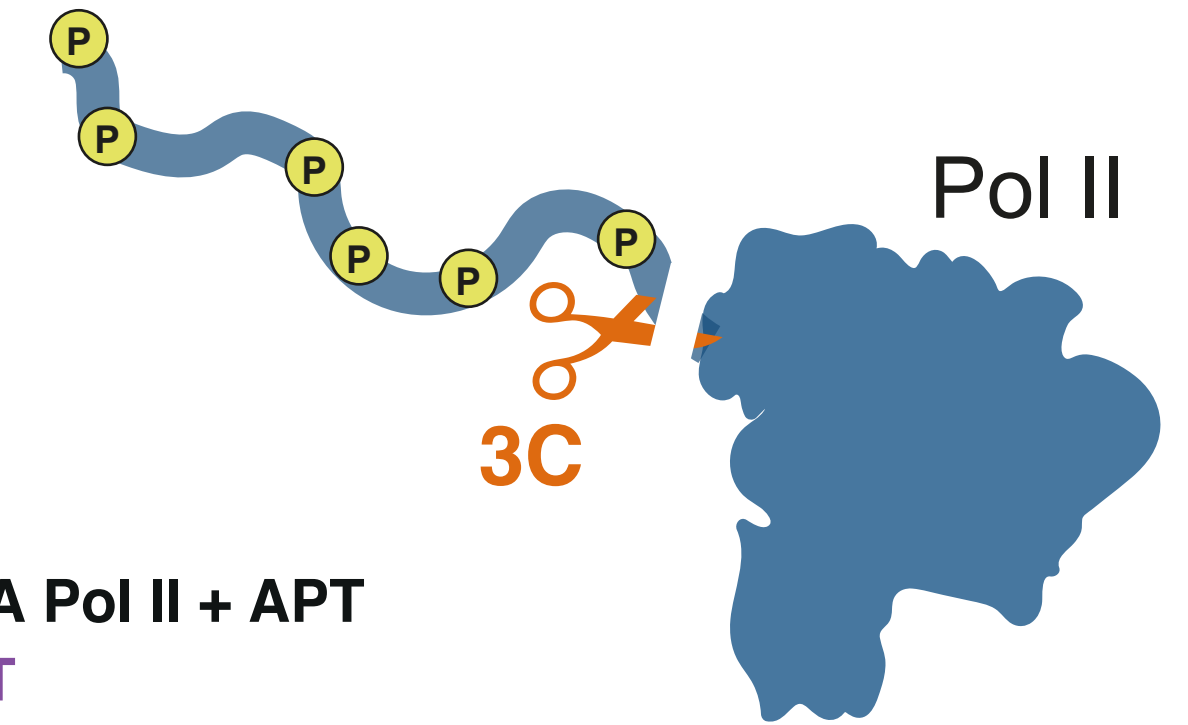


Phosphatase module is necessary and sufficient for the interaction

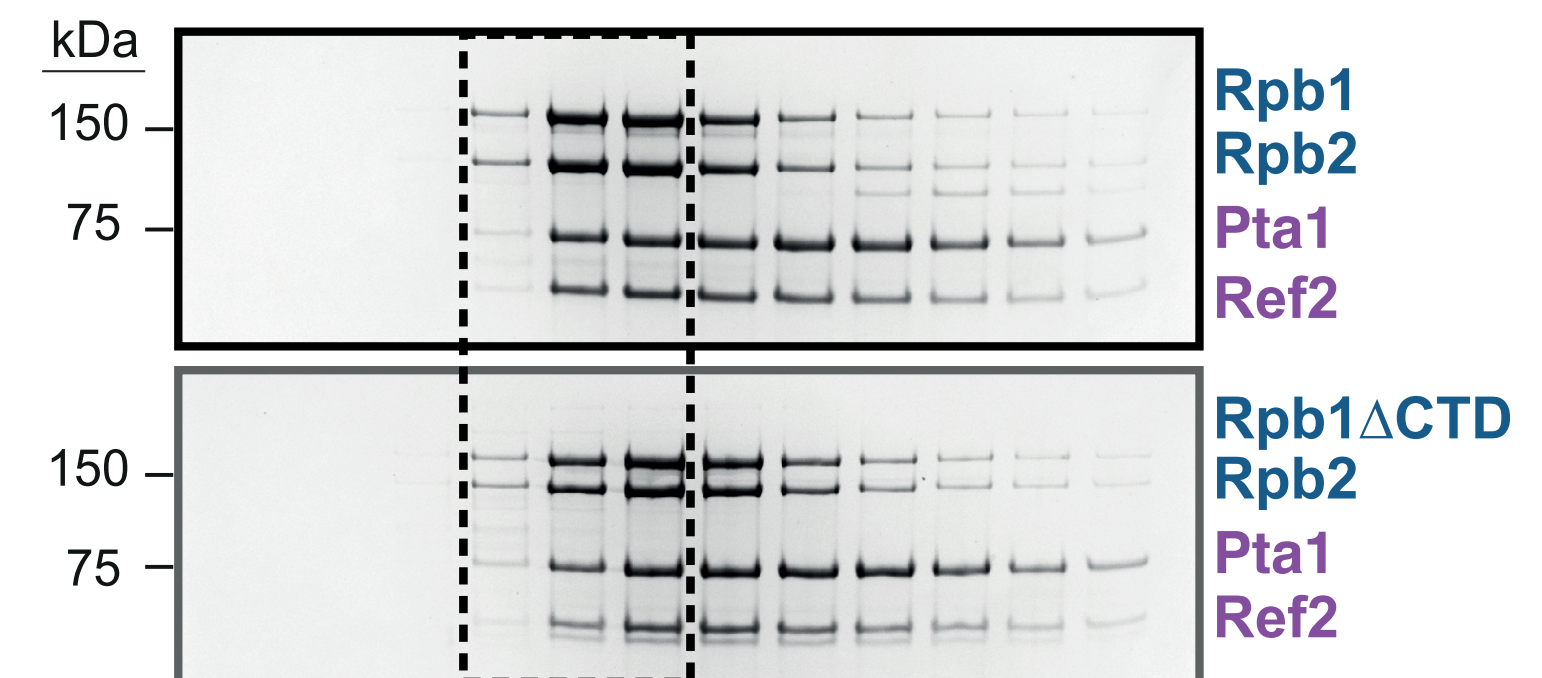
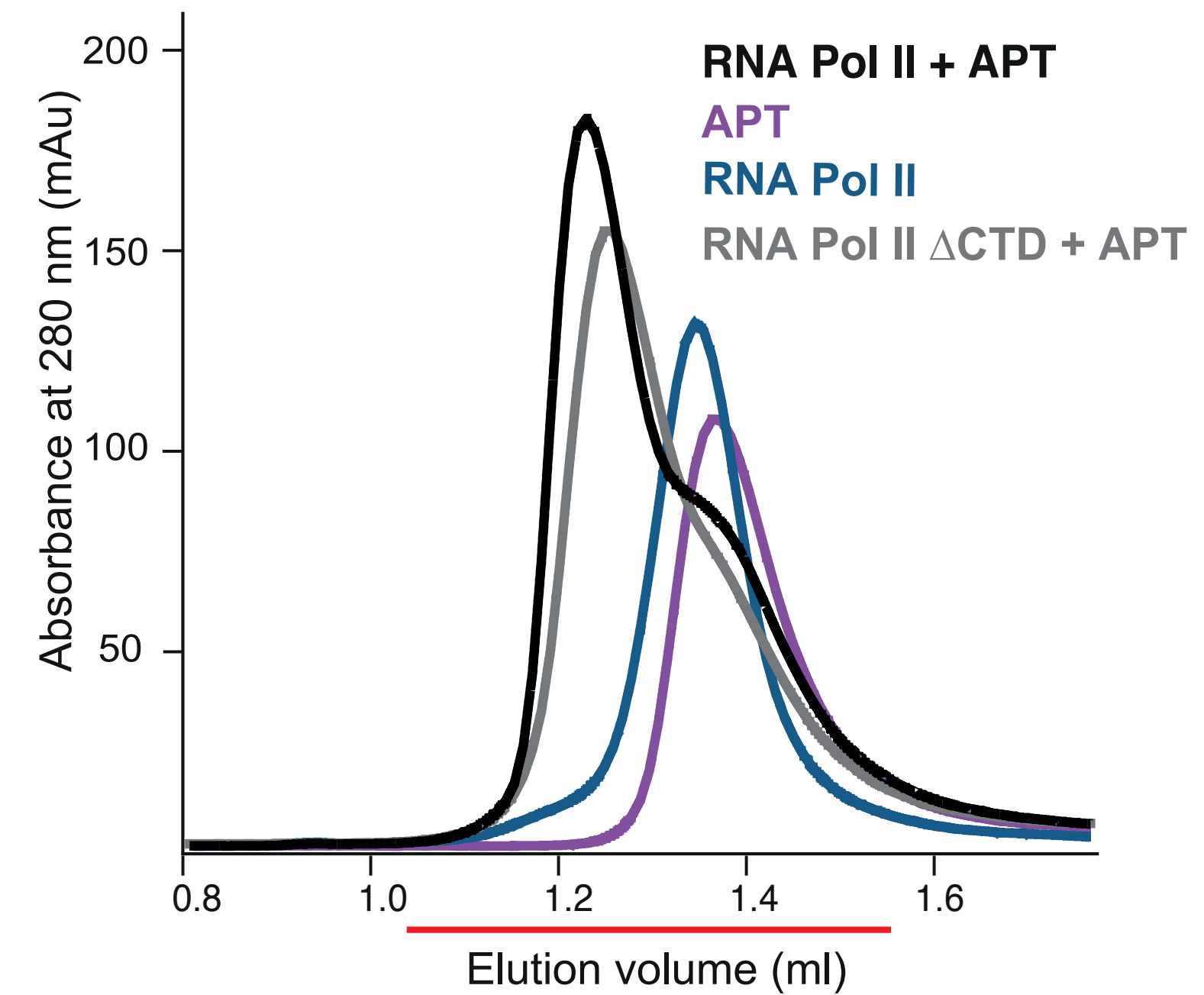
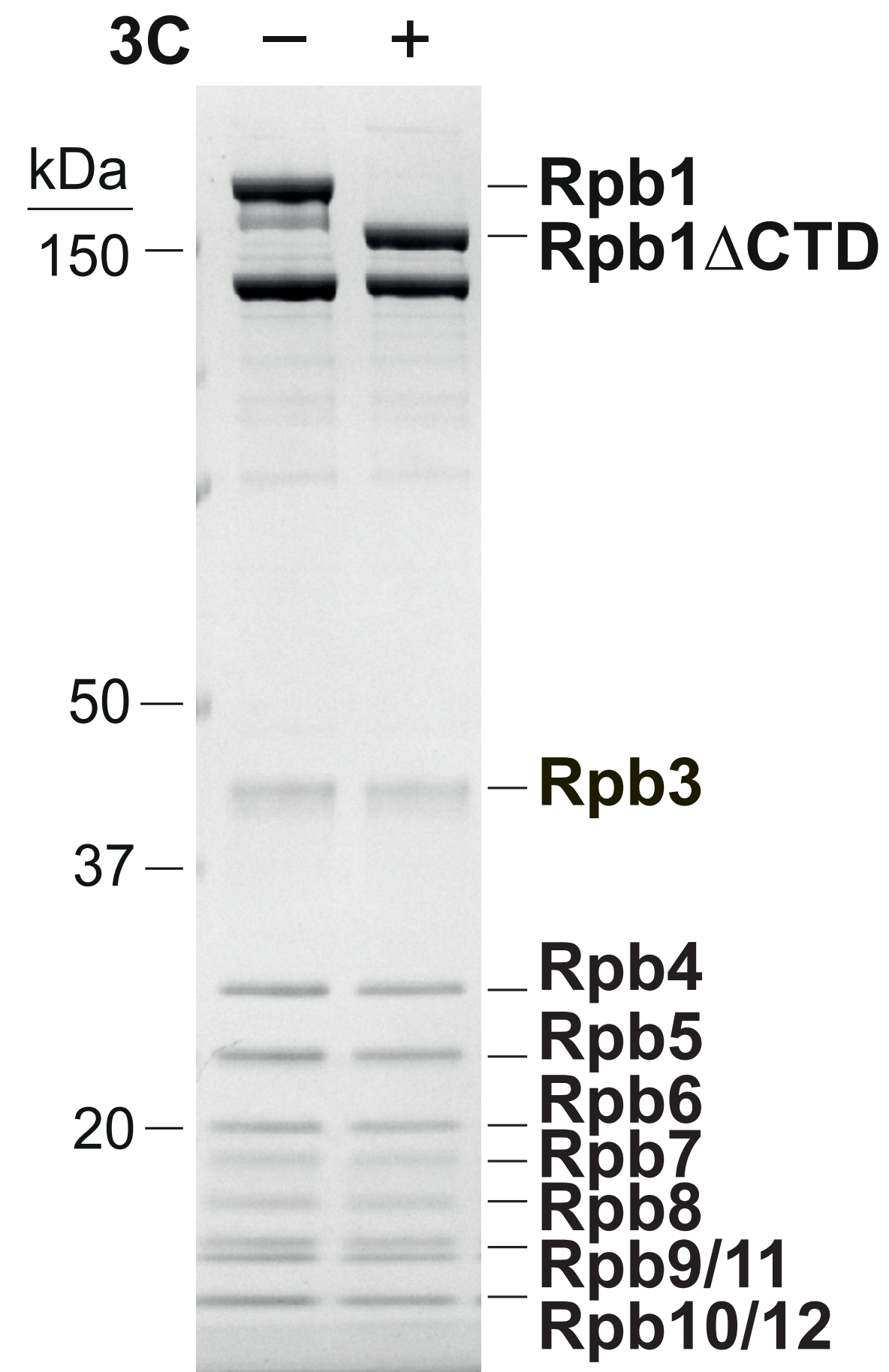
CPF and APT interact directly with Pol II



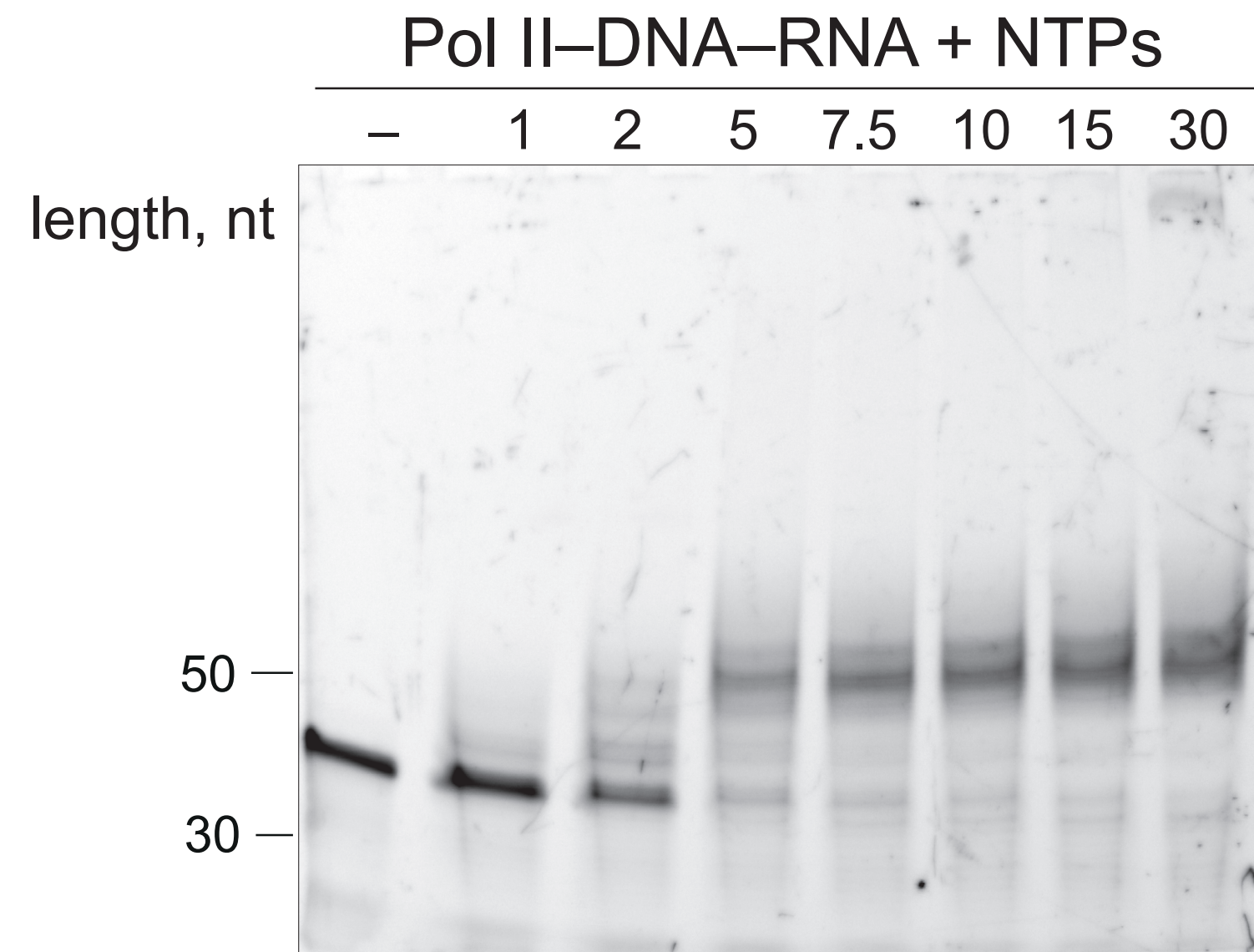
Pol II CTD is not required



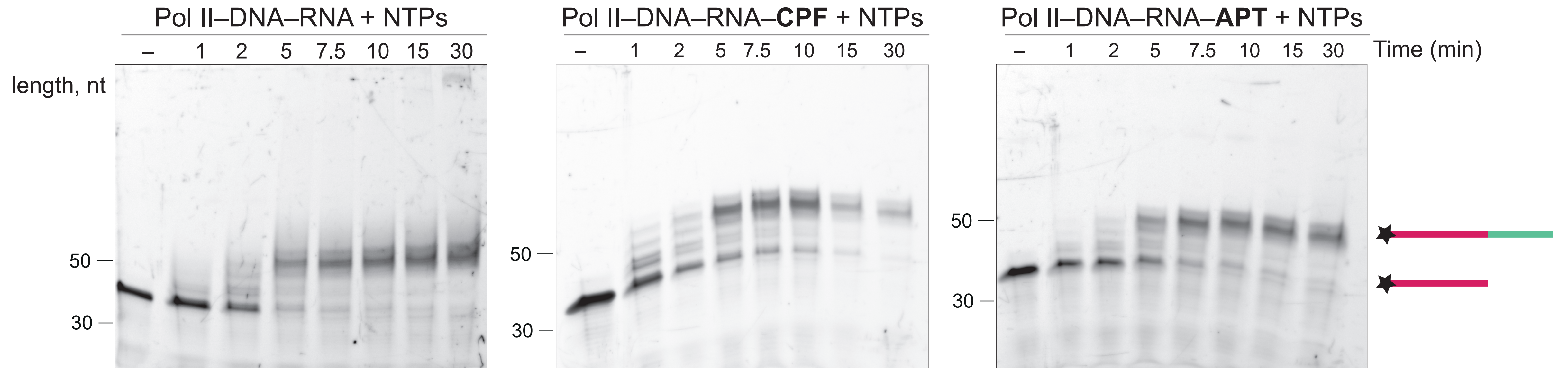
Pol II CTD is not required



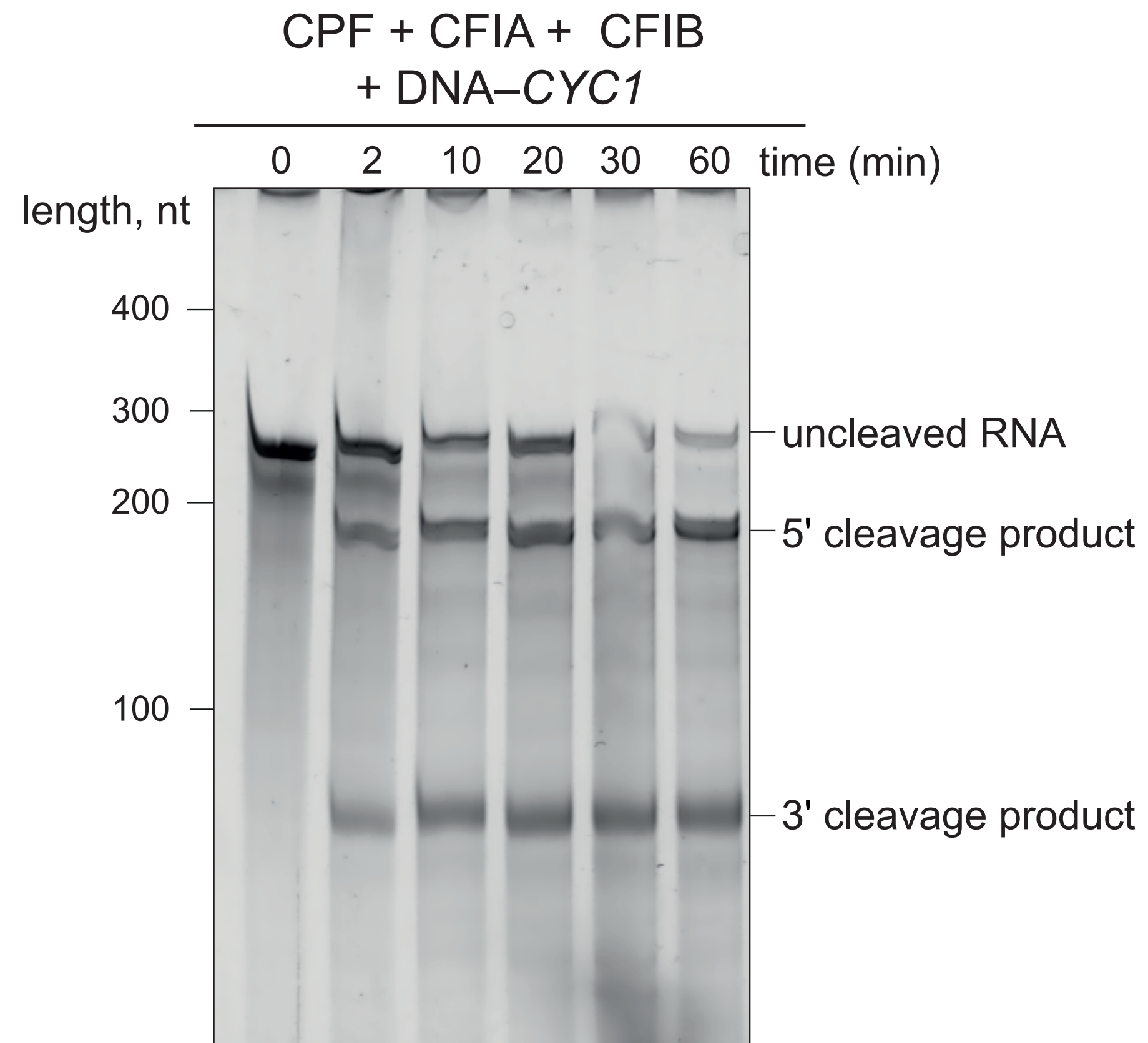
In vitro transcription is compatible with APT/CPF



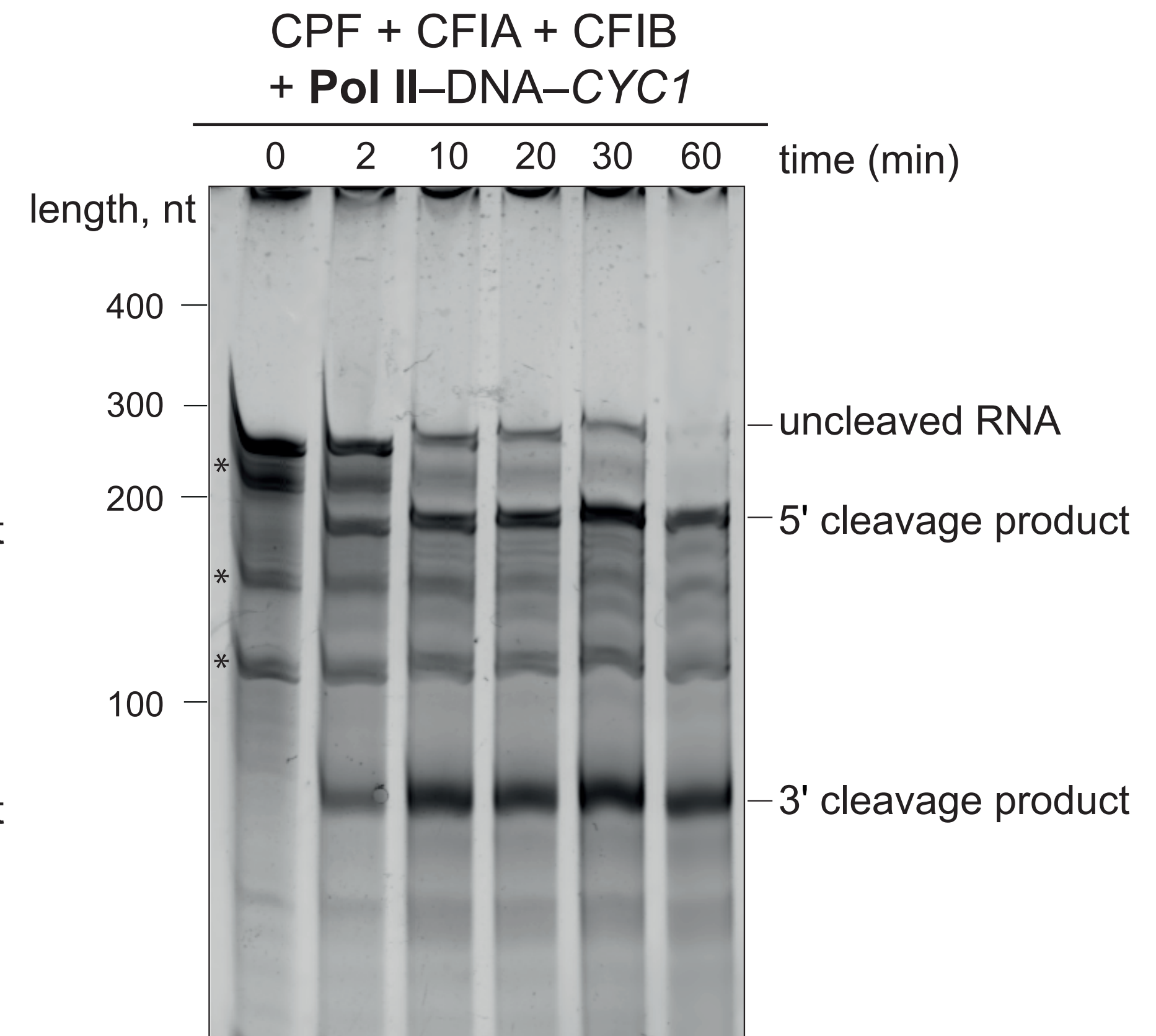
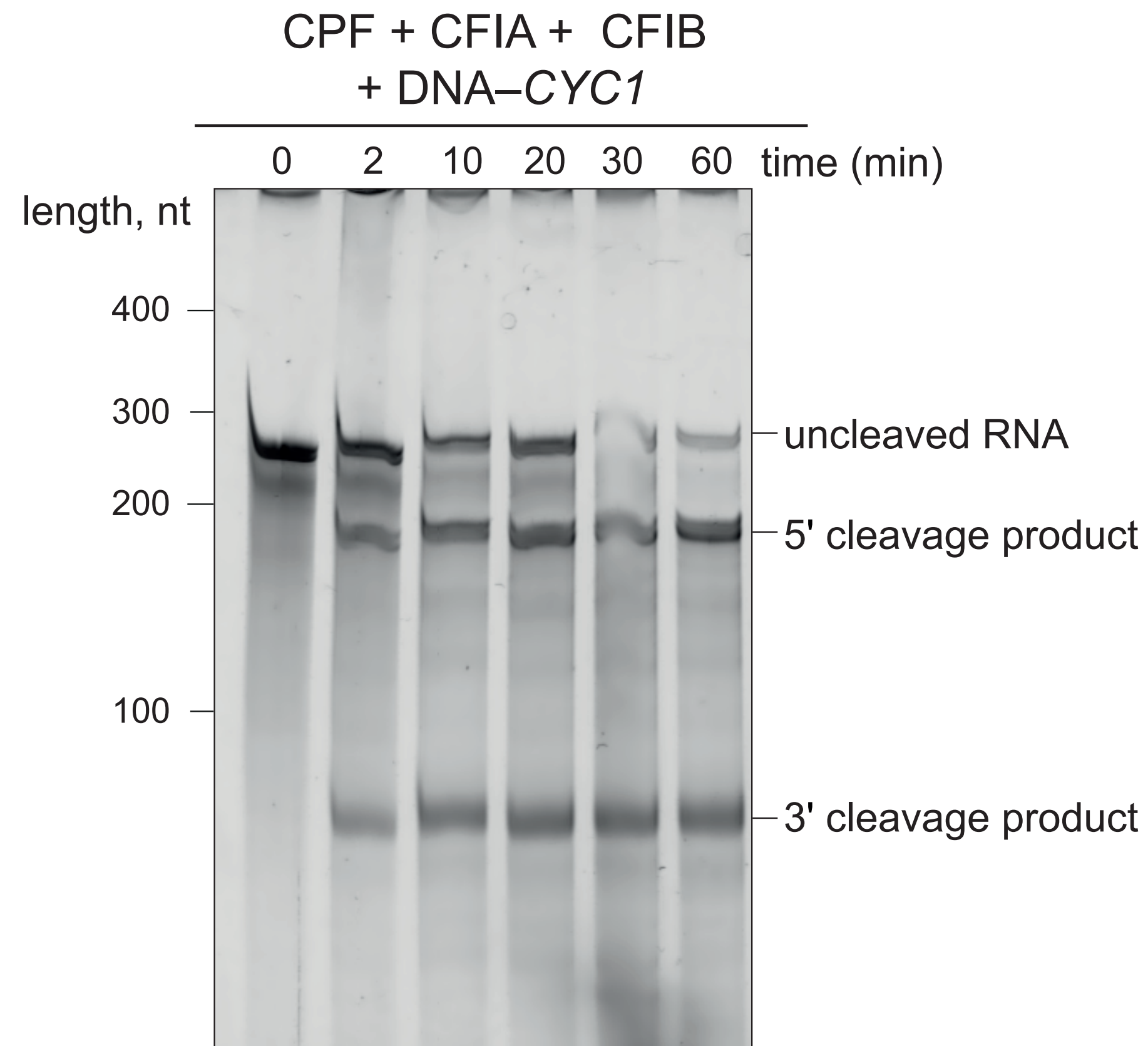
In vitro transcription is compatible with APT/CPF



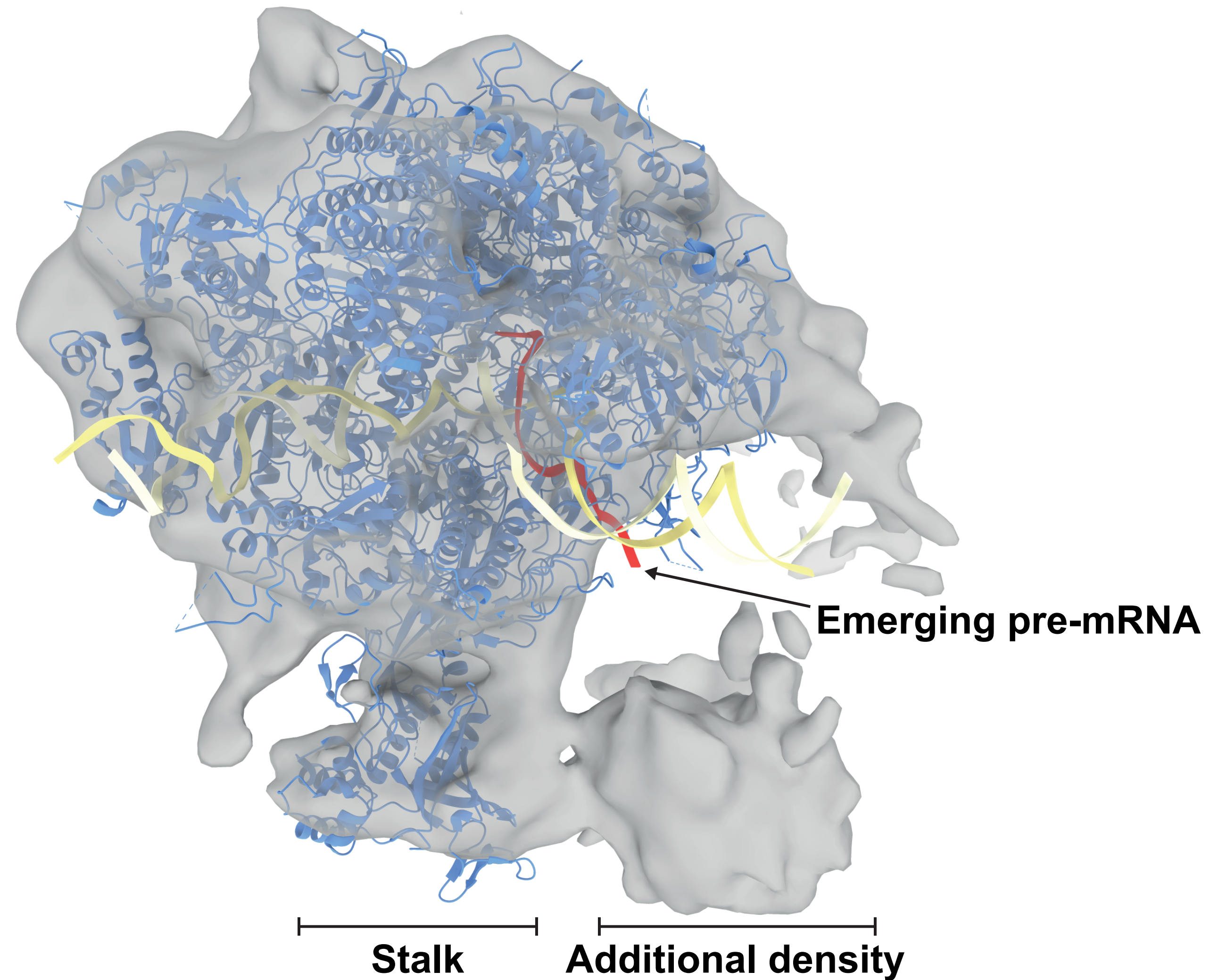
CPF is not stimulated by Pol II



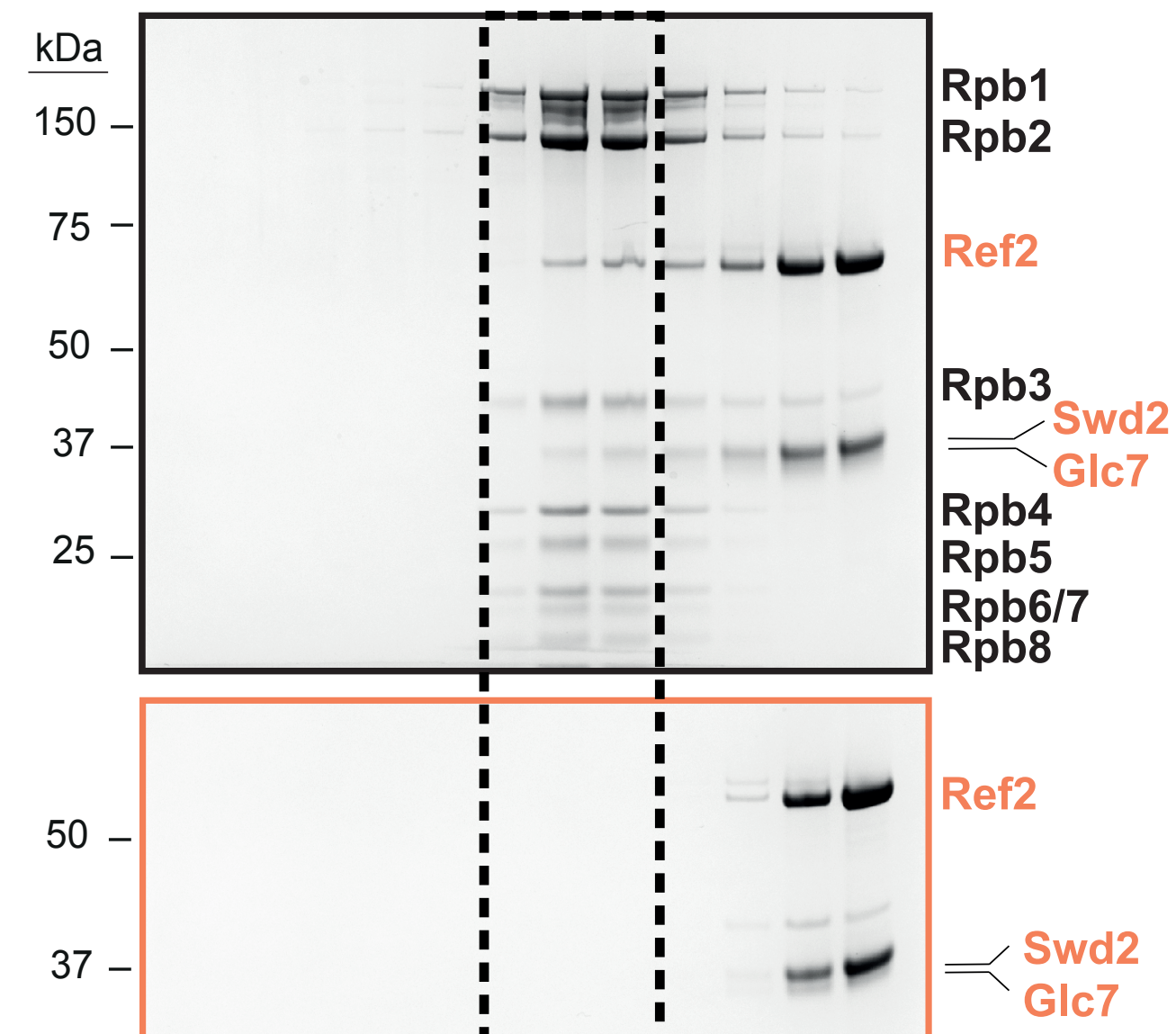
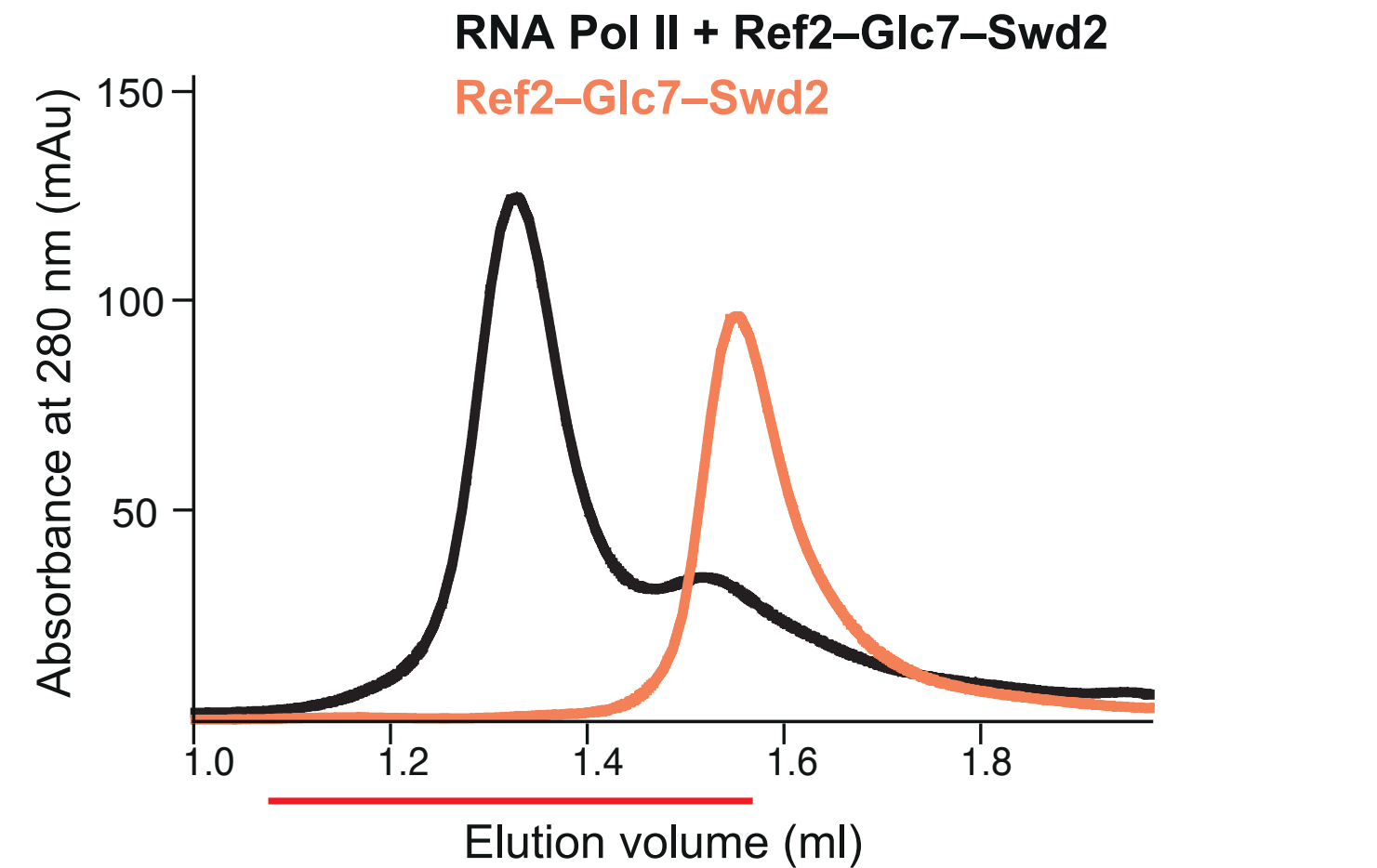
CPF is not stimulated by Pol II



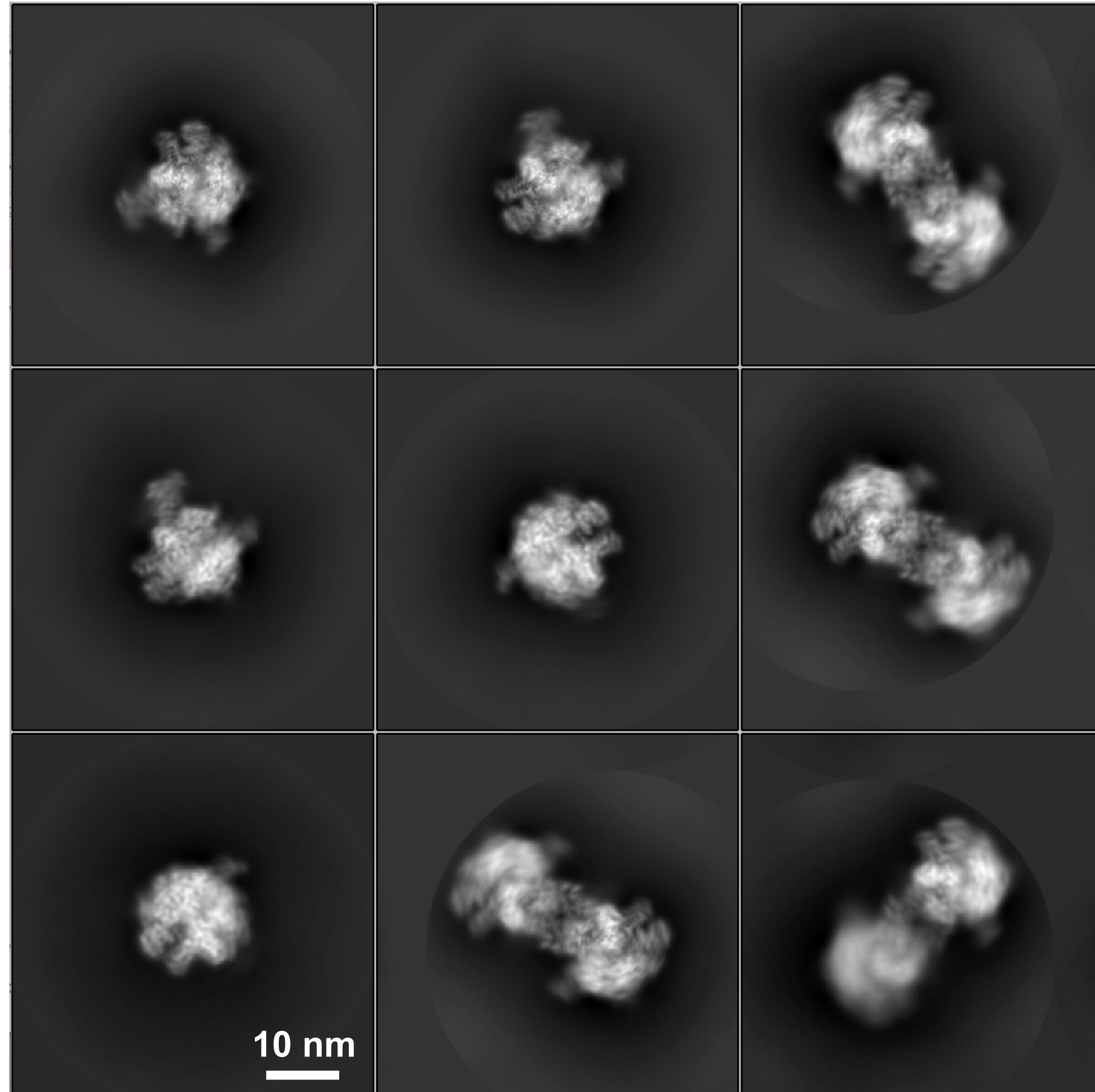
APT interacts directly with Pol II



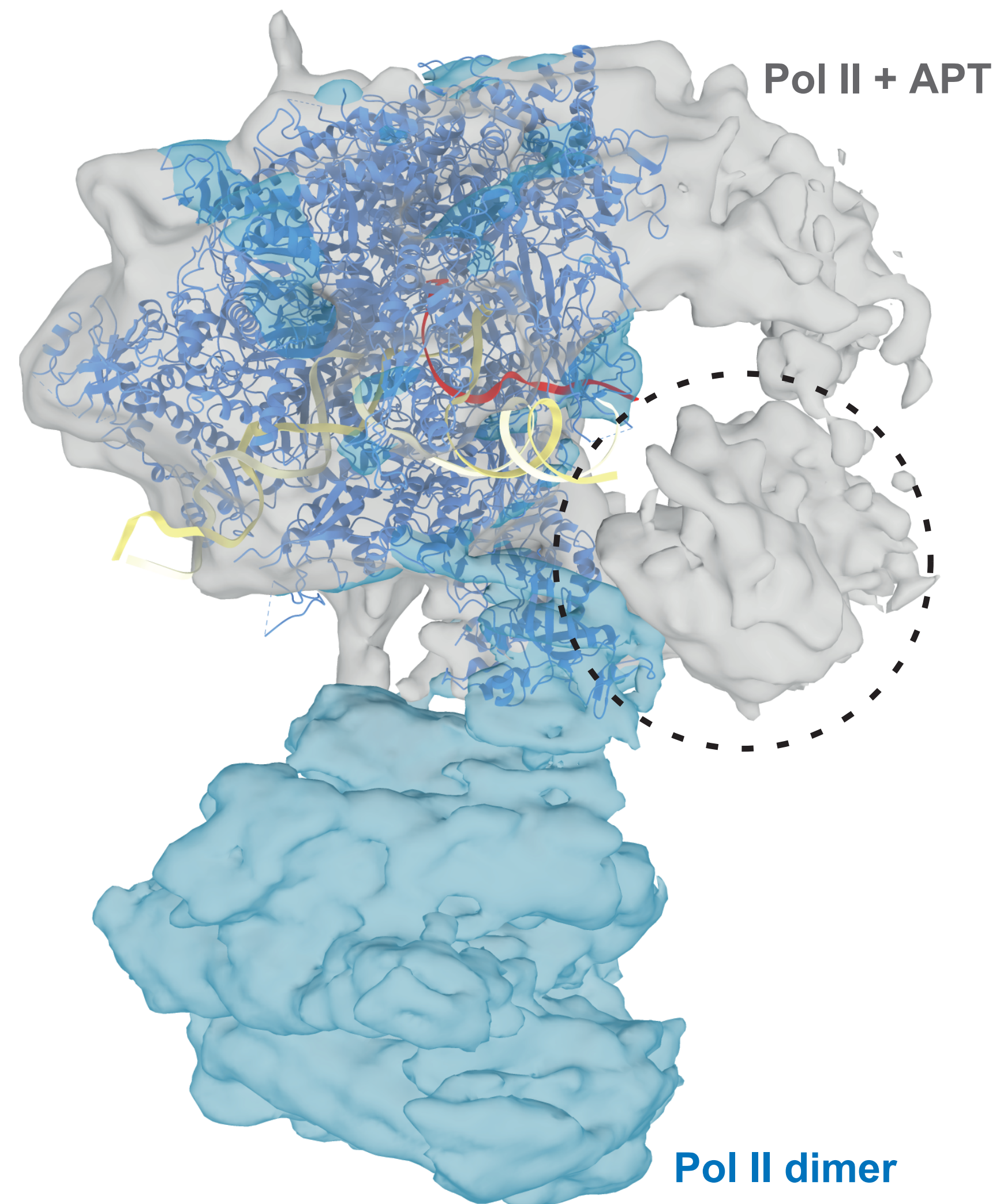
Ref2-Glc7-Swd2 sub complex also interacts with Pol II



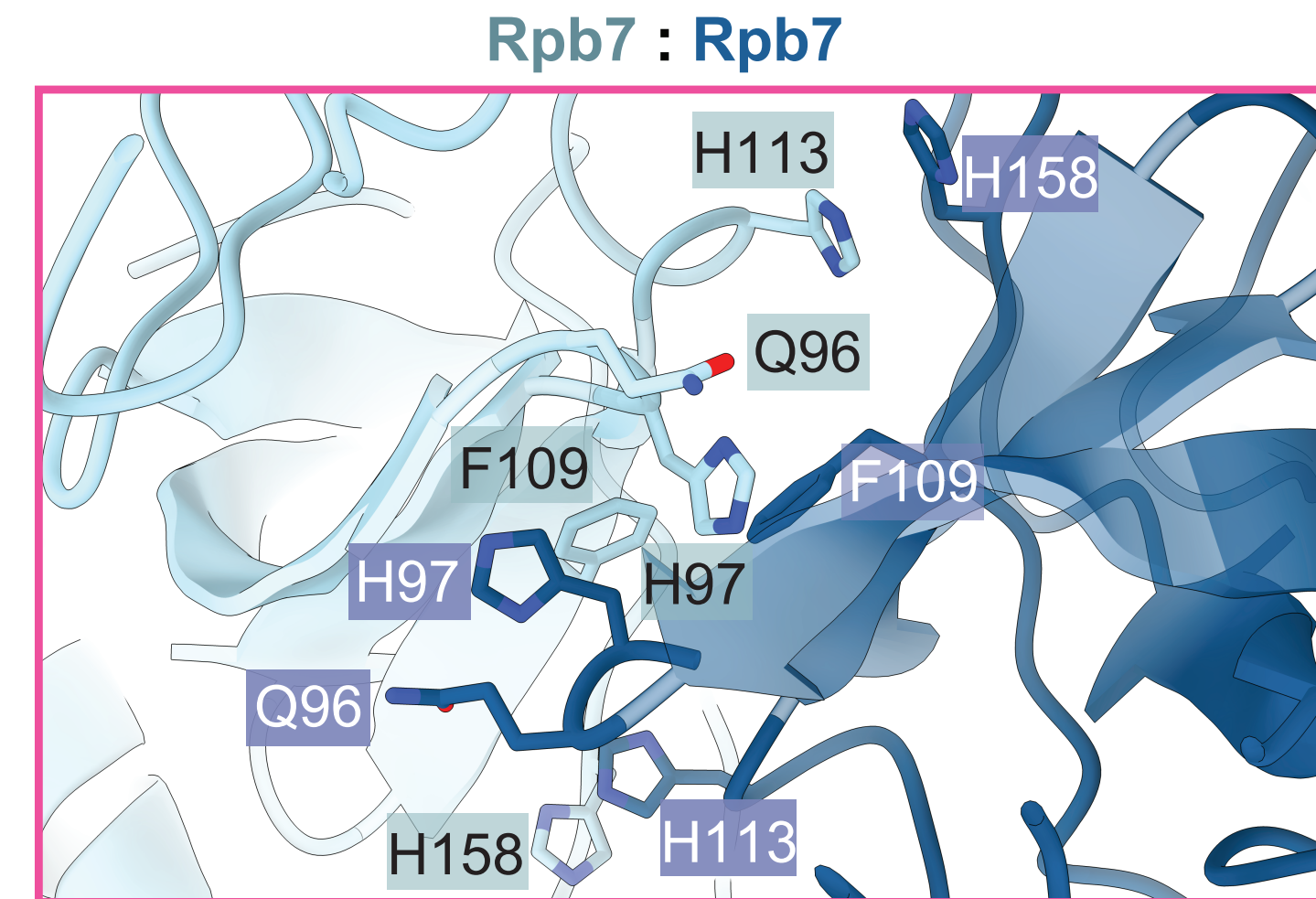
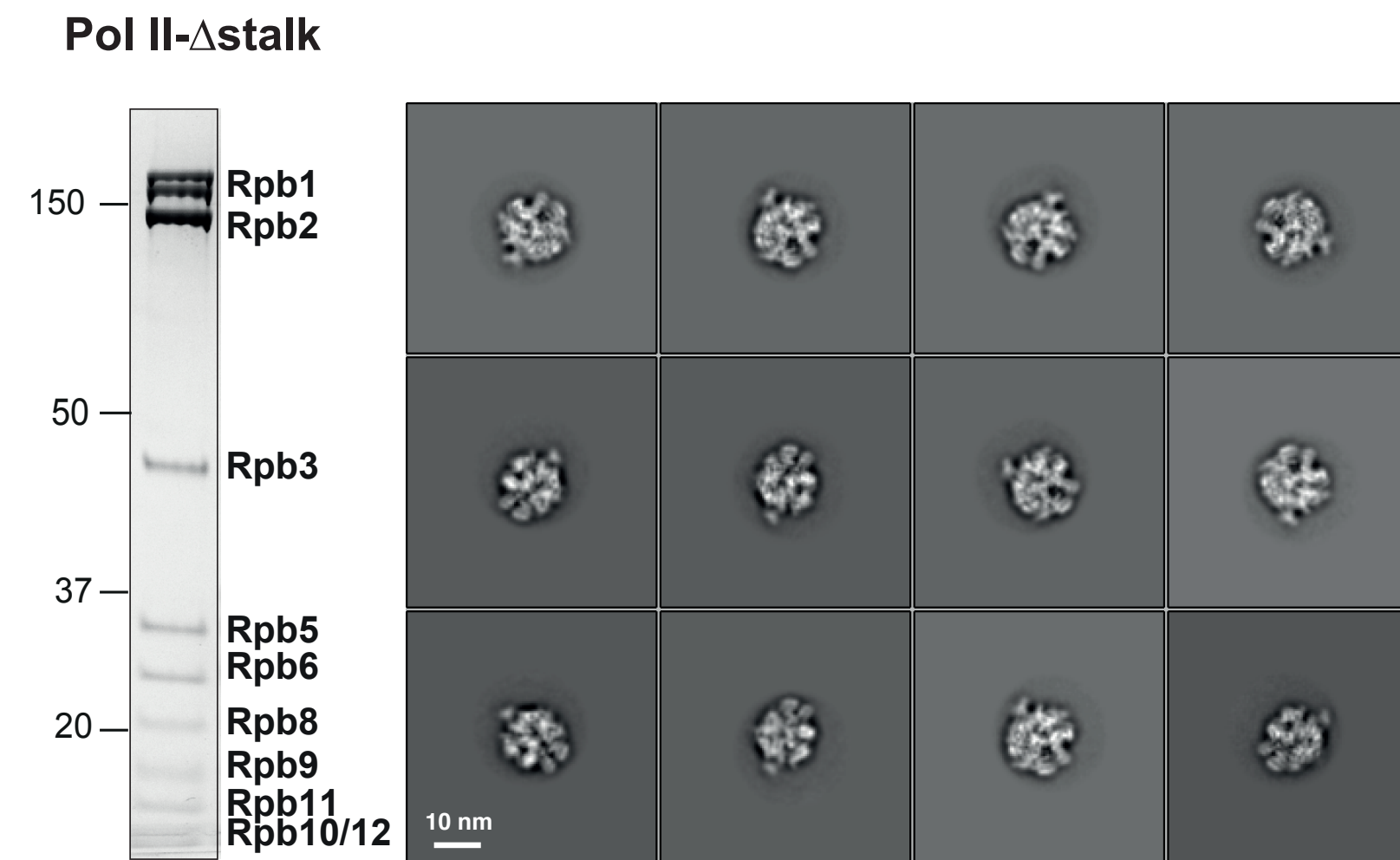
CPF promotes dimerisation of Pol II



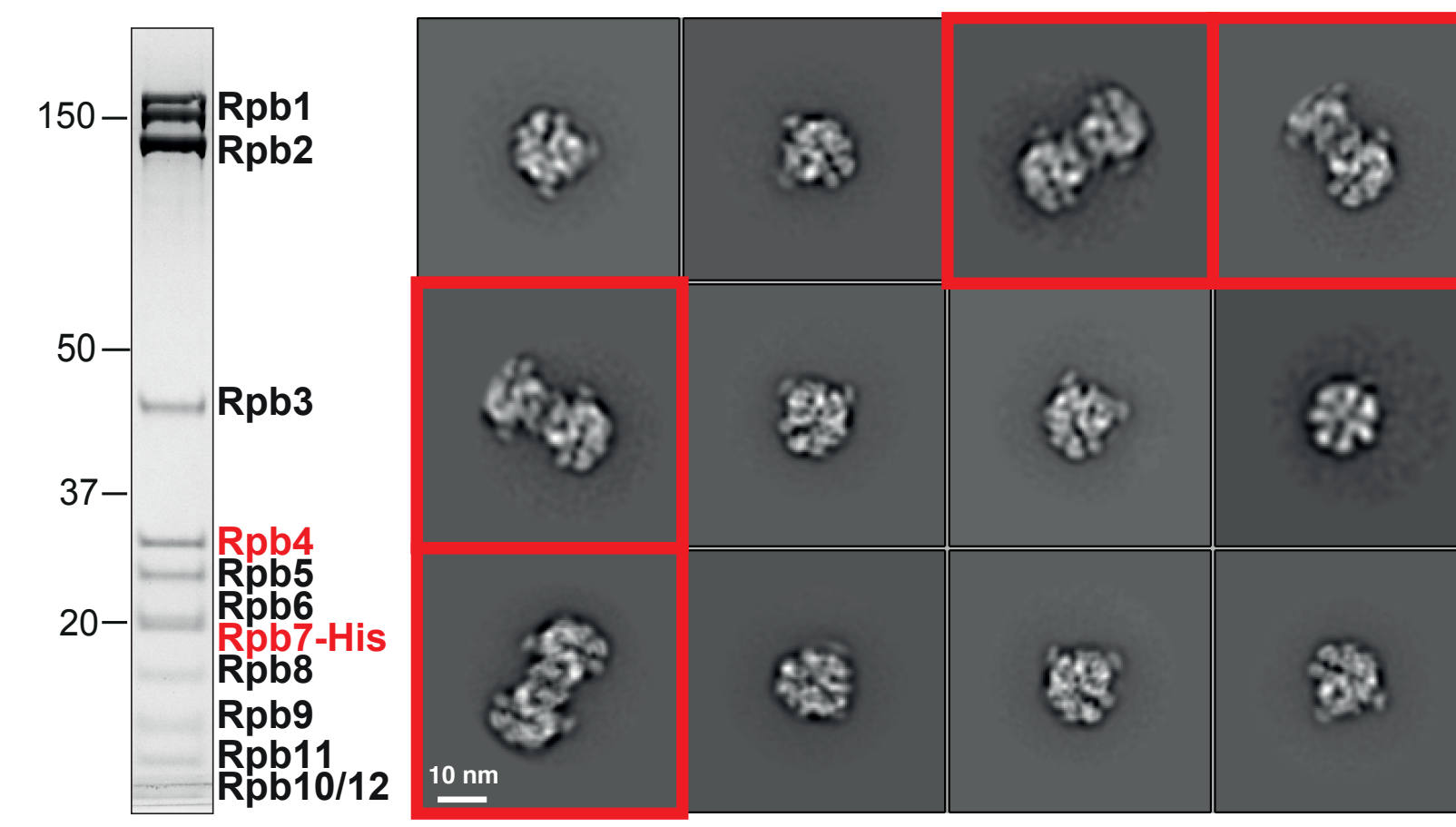
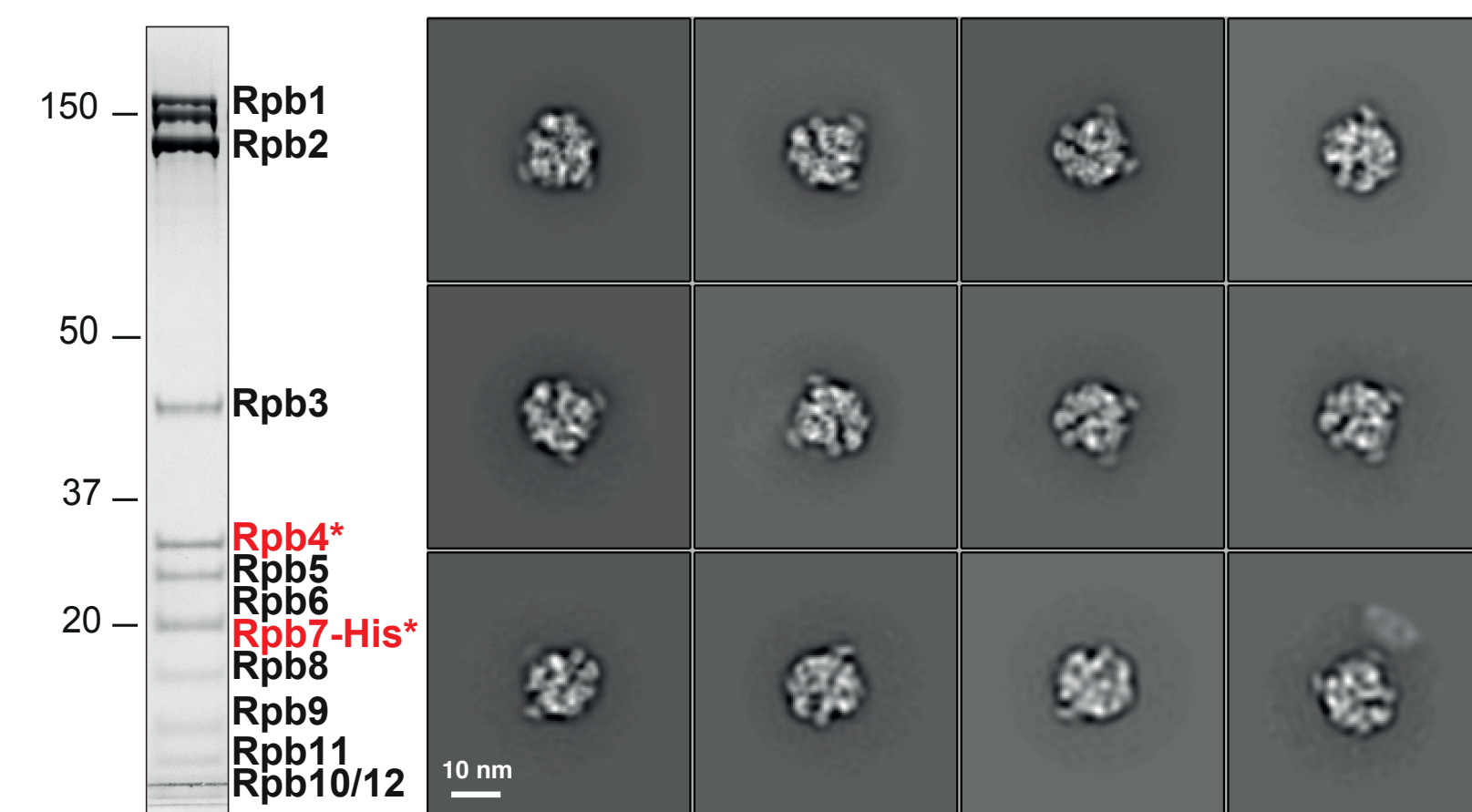
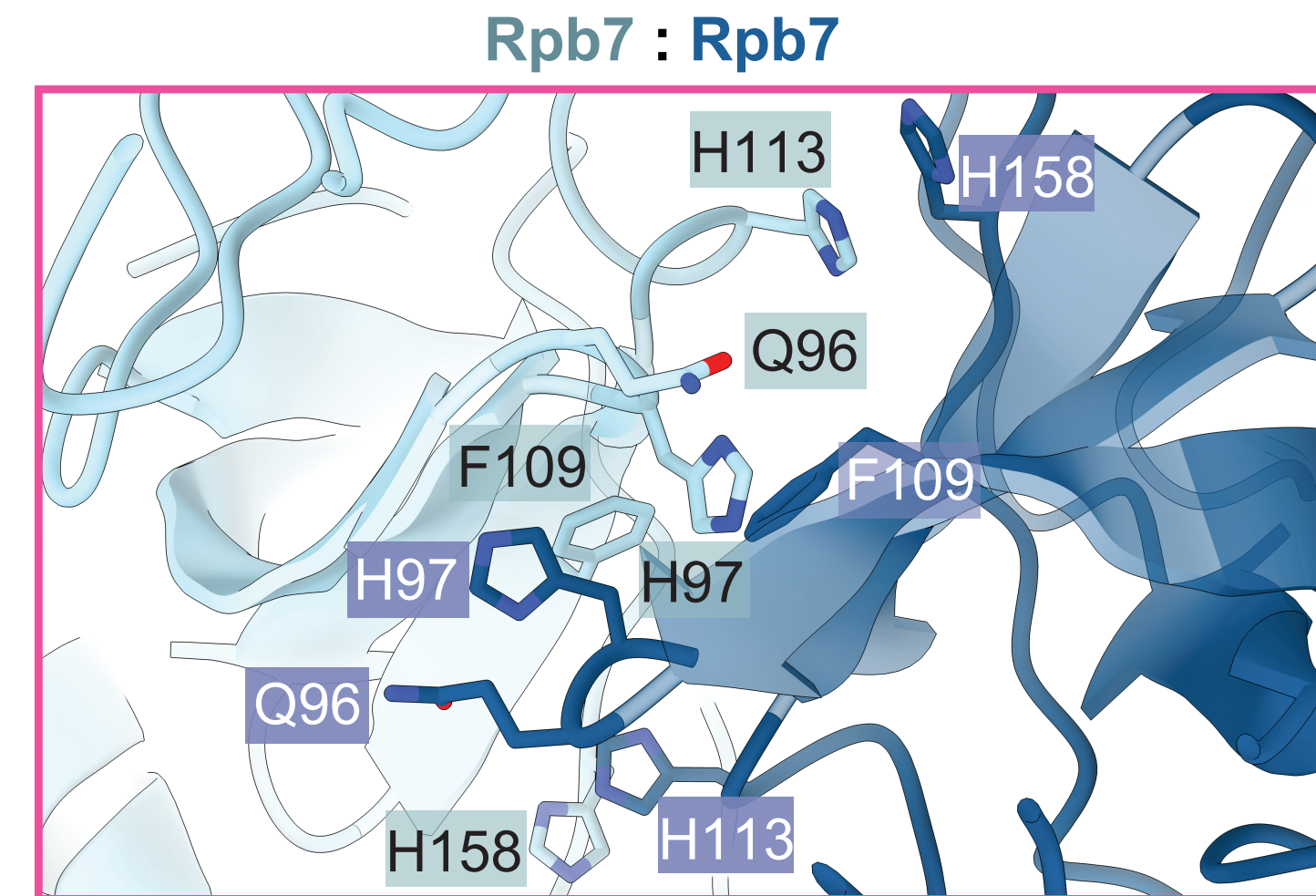
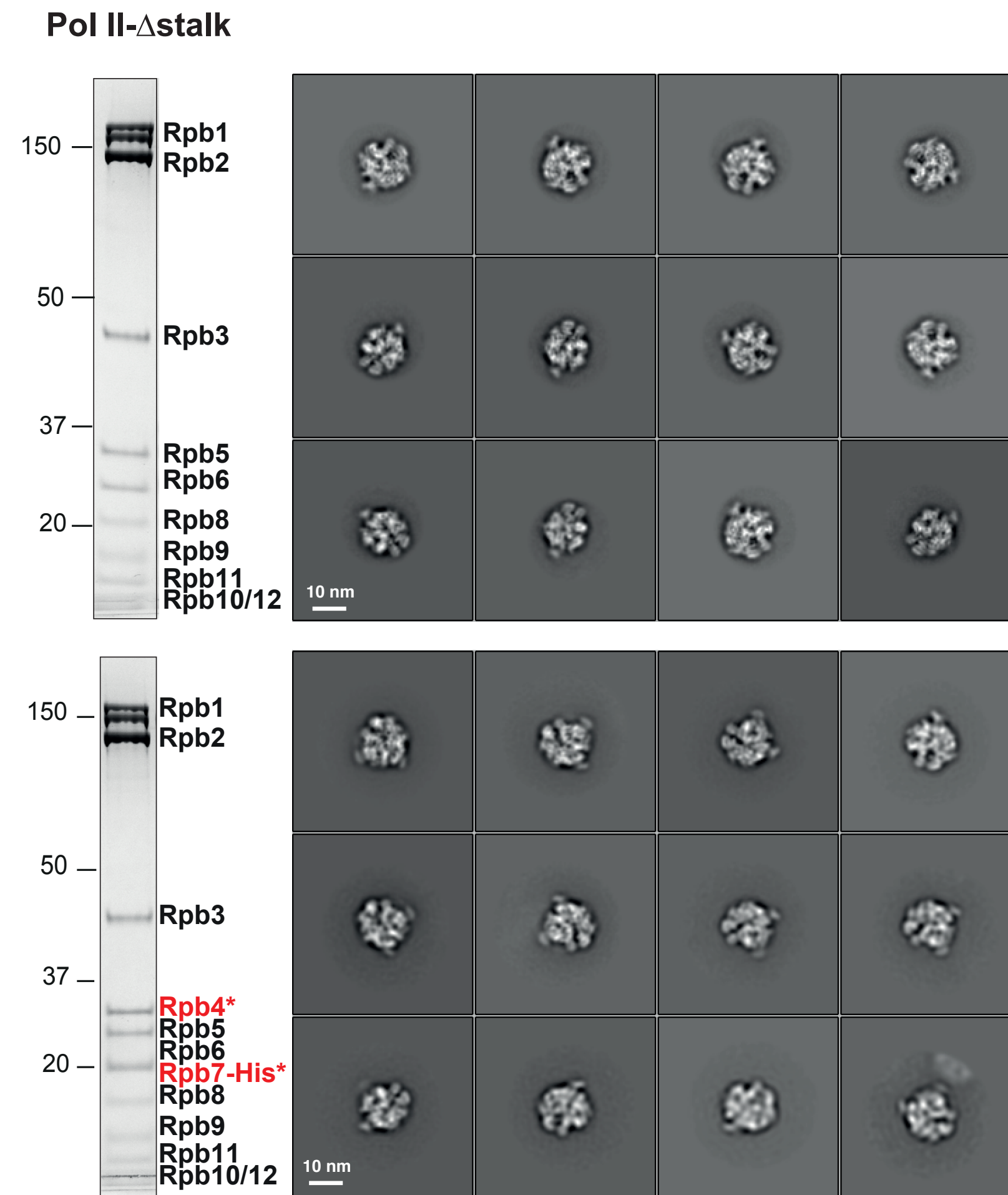
The Pol II dimer is compatible with APT binding



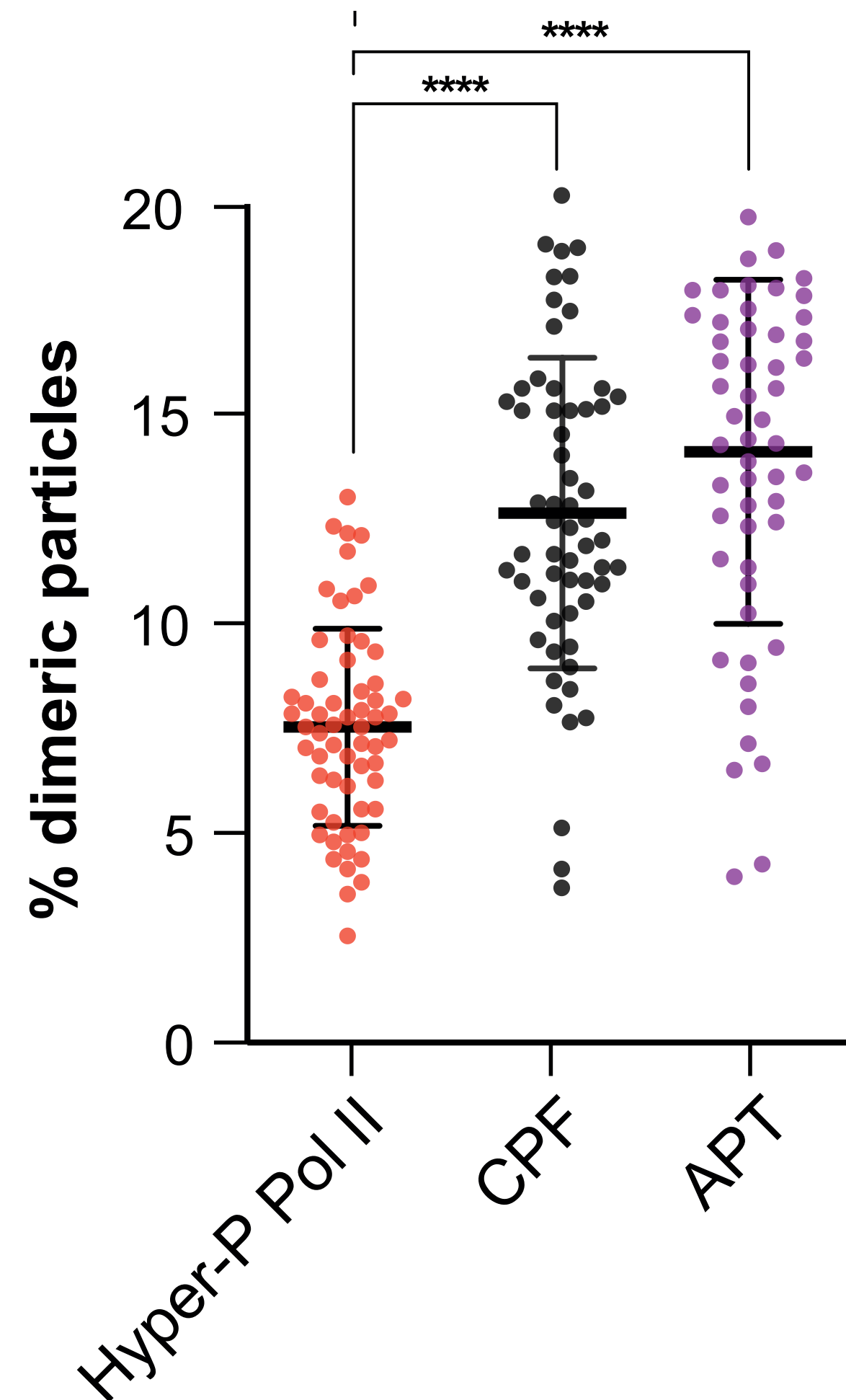
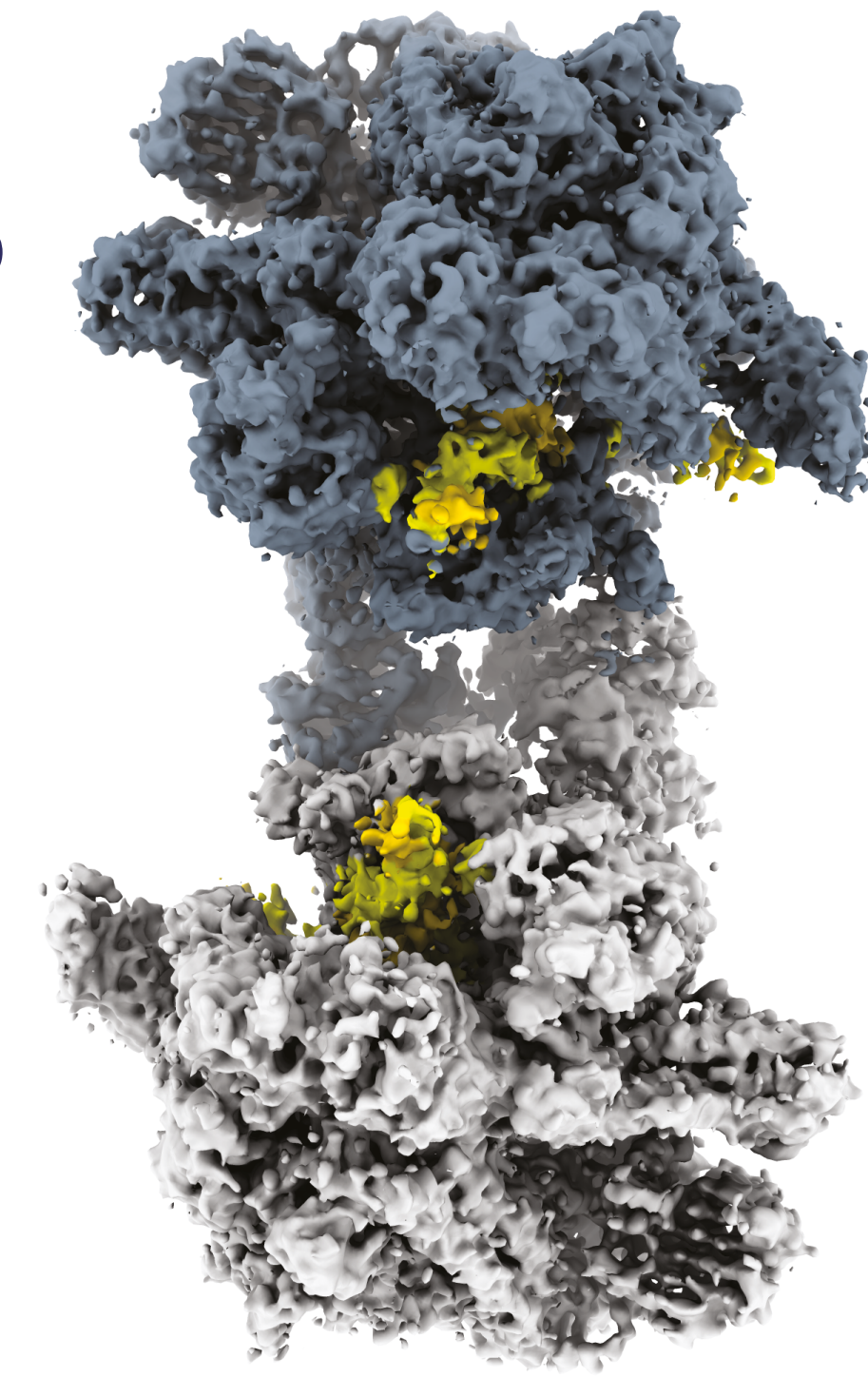
The Pol II stalk is required for dimer formation



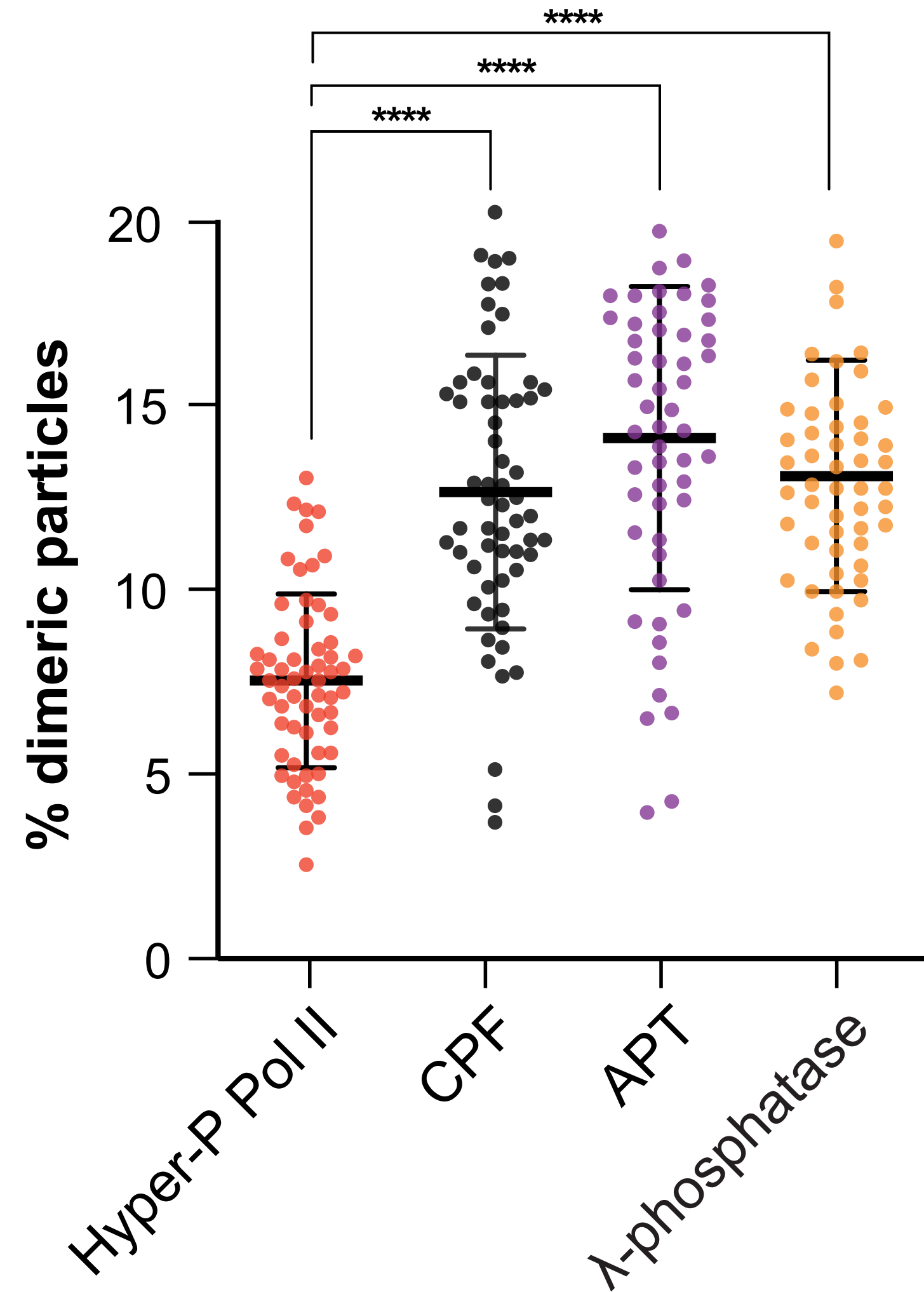
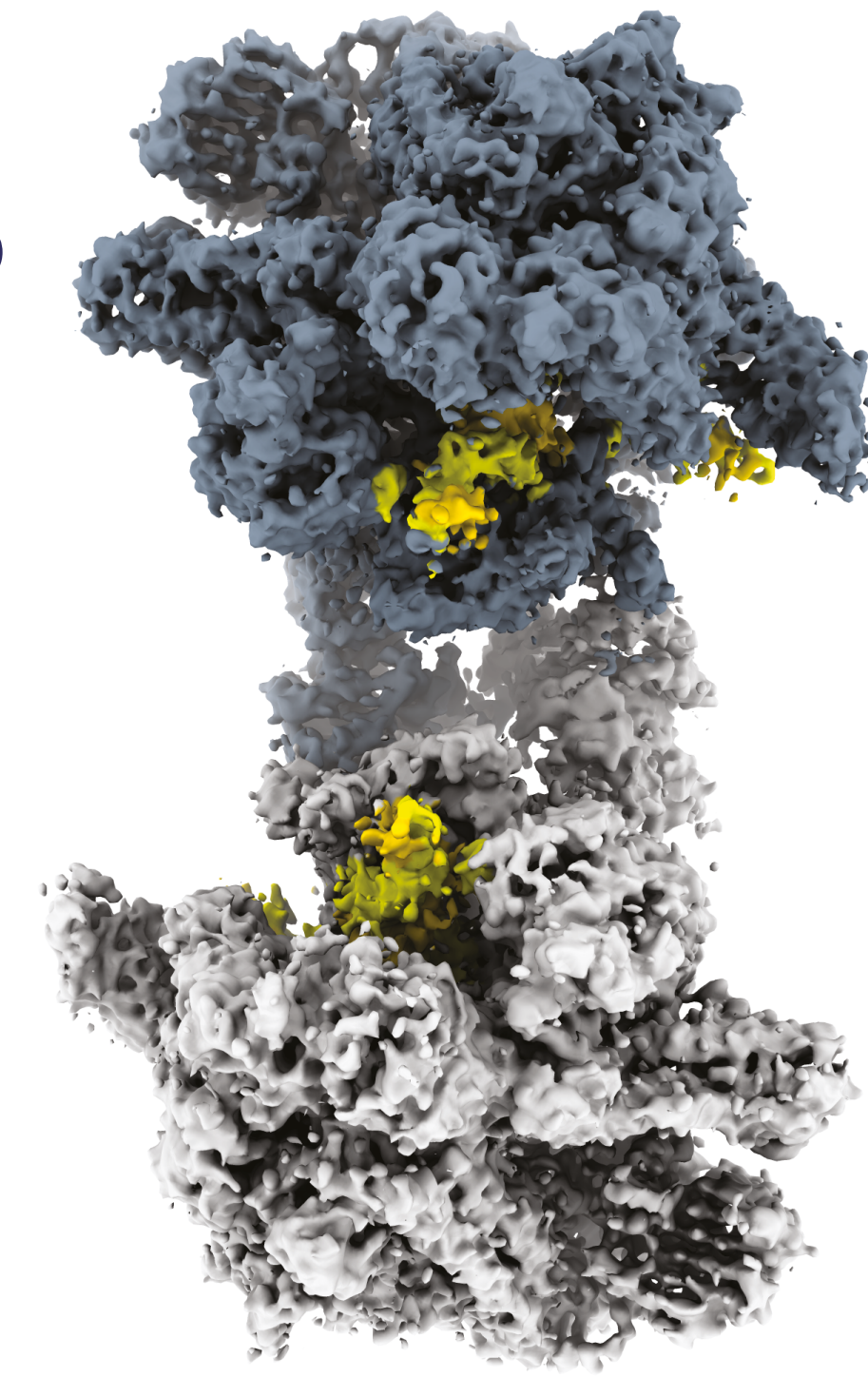
The Pol II stalk is required for dimer formation



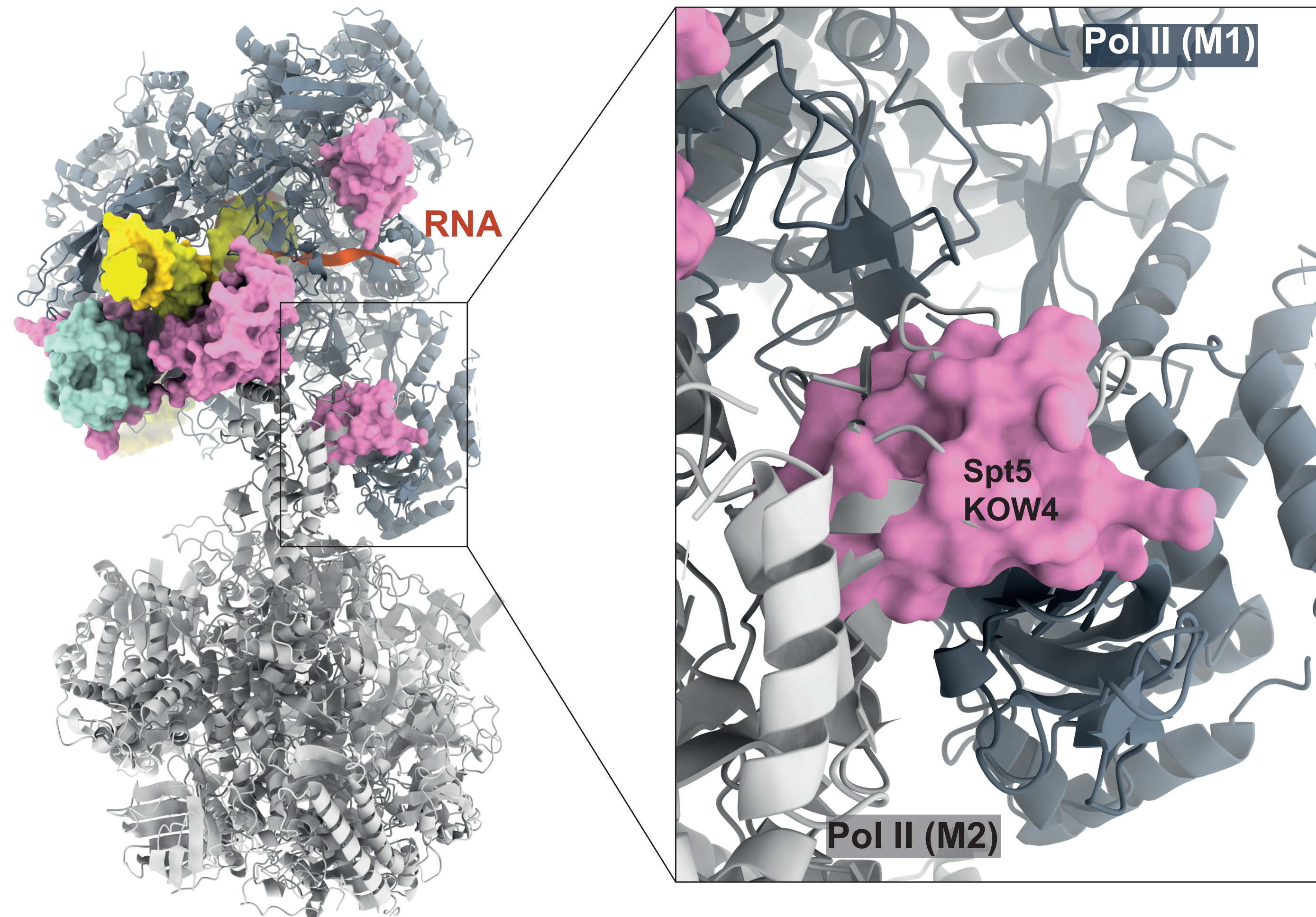
CTD dephosphorylation promotes Pol II dimerization



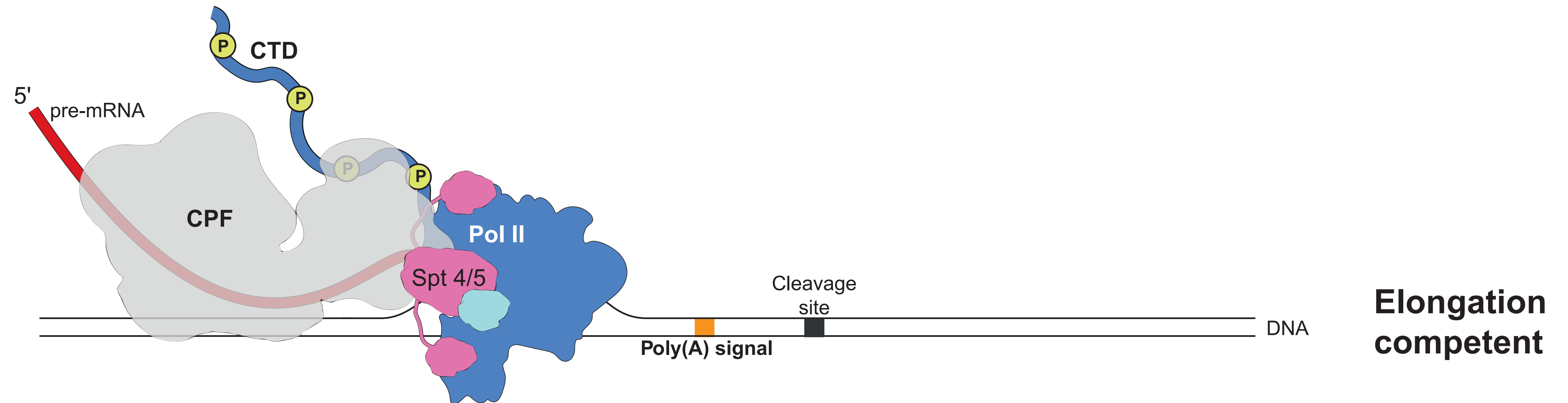
CTD dephosphorylation promotes Pol II dimerization



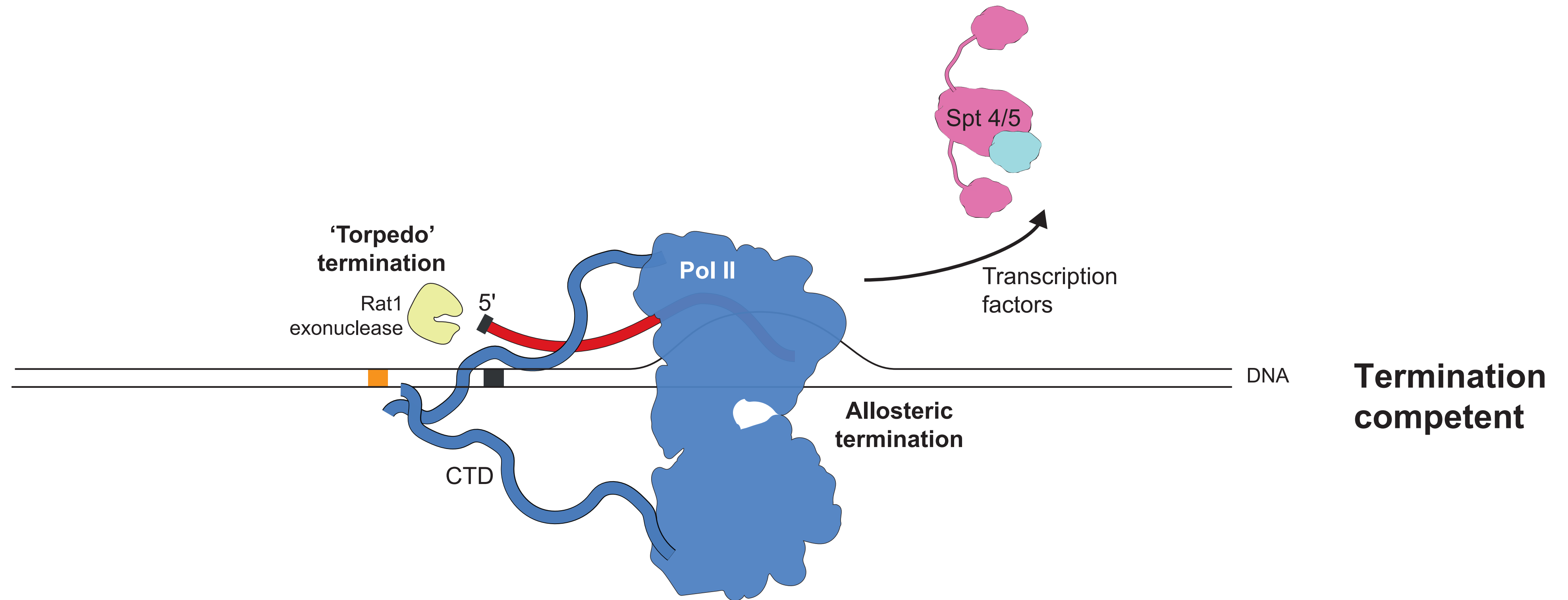
The Pol II dimer clashes with transcription factors



Model for transcription termination



Model for transcription termination



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